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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 111028

TO: Minh-Tam Davis
Location: CM-1 8A01
Art Unit: 1642
Tuesday, December 30, 2003

Case Serial Number: 10/066179

From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes

Examiner Davis,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
CM-1, Rm. 6-A-06
605-1155

mary jane ruhl
9/1996

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111028

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Wednesday, December 24, 2003 4:09 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subj ct: RE: Rush search request for 10066179

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

Fr m: Davis, Minh-Tam
Sent: Wednesday, December 24, 2003 3:53 PM
To: Chan, Christina
Subject: Rush search request for 10066179

Please search in commercial database, PGPUB, issued patent files and interference
SEQ ID NO:1 and 2
Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 8A01, MB 8E12
305-2008

#73622

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: December 29, 2003, 23:29:49 ; Search time 29 Seconds
(without alignments)
245.111 Million cell updates/sec

Title: US-10-066-179-2

Perfect score: 905
Sequence: 1 MFOIPEFPESEDESSAER.....RVFQSWMDRLGRSSAPQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	905	100.0	168	2	US-08-717-123-2
2	905	100.0	168	3	US-08-985-335-1
3	905	100.0	168	4	US-09-410-372-1
4	905	100.0	168	4	US-09-375-257-2
5	751	83.0	166	1	US-08-665-617-2
6	744	82.2	168	3	US-08-985-335-7
7	744	82.2	168	3	US-09-410-372-7
8	649	71.7	204	1	US-08-333-565-2
9	649	71.7	204	2	US-08-661-479-2
10	649	71.7	204	2	US-08-733-505A-1
11	646	71.4	204	2	US-08-733-505A-12
12	646	71.4	204	2	US-08-733-505A-13
13	646	71.4	204	2	US-08-717-123-3
14	646	71.4	204	2	US-09-375-257-3
15	643	71.0	204	2	US-08-733-505A-14
16	314	34.4	59	2	US-08-733-505A-55
17	311	34.4	59	2	US-08-733-505A-56
18	311	34.4	59	2	US-08-733-505A-57
19	308	34.0	59	2	US-08-733-505A-58
20	116	12.8	23	1	US-08-333-565-10
21	116	12.8	23	2	US-08-661-479-10
22	103.5	11.4	265	4	US-09-252-991A-21368
23	103	11.4	215	4	US-09-252-991A-32685
24	101	11.2	467	4	US-09-252-991A-18296
25	100.5	11.1	429	4	US-09-252-991A-29079
26	98.5	10.9	517	4	US-09-252-991A-21294
27	97	10.7	229	4	US-09-252-991A-32515

28	97	10.7	2509	2	US-08-149-097D-35	Sequence 35, Appl
29	96.5	10.7	217	4	US-09-252-991A-24818	Sequence 24818, A
30	96.5	10.7	1182	3	US-09-041-886-21	Sequence 21, Appl
31	95	10.5	377	4	US-09-252-991A-20479	Sequence 20479, A
32	95	10.5	649	4	US-09-252-991A-29726	Sequence 29726, A
33	94.5	10.4	451	4	US-09-252-991A-27602	Sequence 27602, A
34	94	10.4	494	4	US-09-252-991A-32449	Sequence 32449, A
35	94	10.4	571	4	US-09-252-991A-28760	Sequence 28760, A
36	94	10.4	731	4	US-09-252-991A-35890	Sequence 35890, A
37	92.5	10.2	421	4	US-09-252-991A-32326	Sequence 32326, A
38	92.5	10.2	1402	4	US-09-125-635-12	Sequence 12, Appl
39	92	10.2	193	4	US-09-252-991A-37357	Sequence 27357, A
40	91.5	10.1	284	4	US-09-252-991A-20213	Sequence 20213, A
41	91.5	10.1	625	4	US-09-252-991A-19871	Sequence 19871, A
42	90.5	10.0	152	4	US-09-252-991A-24730	Sequence 24730, A
43	90.5	10.0	345	4	US-09-252-991A-18076	Sequence 18076, A
44	90.5	10.0	395	4	US-09-252-991A-26116	Sequence 26116, A
45	90	9.9	288	4	US-09-252-991A-27676	Sequence 27676, A

ALIGNMENTS

RESULT 1
US-08-717-123-2
Sequence 2, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-717-123-2
Query Match 100.0%; Score 905; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 6,7e-86;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFOIPEFPESEDESSAERGLGSPAGDGGSGGKRRQPGILMDASHOQOPTSSSH 60
DB 1 MFOIPEFPESEDESSAERGLGSPAGDGGSGGKRRQPGILMDASHOQOPTSSSH 60
QY 61 HCGAGAVEIRSRHSSYPAGTEDEGMCGBEPSPFRGRSRAPNIMAAQRVGRLEIRMSDE 120

Db 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPNNLMAAQRGRELRRMSDE 120
QY 121 FVDSFKKGLPRPKSAGTATQWROSSSWTRVFQSWMDNLRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQWROSSSWTRVFQSWMDNLRGSSAPSQ 168

RESULT 2

US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Puri
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
; US-08-985-335-1

Query Match 100.0%; Score 905; DB 3; Length 168;
Best Local Similarity 100.0%; Pred. No. 6,7e-86;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFPESEDESSAERGLGSPAGDGPSSGSKHROAPGLMDASHOEOPTSSSH 60
Db 1 MFQIPEFPESEDESSAERGLGSPAGDGPSSGSKHROAPGLMDASHOEOPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPNNLMAAQRGRELRRMSDE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPNNLMAAQRGRELRRMSDE 120
QY 121 FVDSFKKGLPRPKSAGTATQWROSSSWTRVFQSWMDNLRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQWROSSSWTRVFQSWMDNLRGSSAPSQ 168

RESULT 3
US-09-410-372-1

; Sequence 1, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Puri
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/410,372
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,335
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
; US-09-410-372-1

Query Match 100.0%; Score 905; DB 3; Length 168;
Best Local Similarity 100.0%; Pred. No. 6,7e-86;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFPESEDESSAERGLGSPAGDGPSSGSKHROAPGLMDASHOEOPTSSSH 60
Db 1 MFQIPEFPESEDESSAERGLGSPAGDGPSSGSKHROAPGLMDASHOEOPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPNNLMAAQRGRELRRMSDE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPNNLMAAQRGRELRRMSDE 120
QY 121 FVDSFKKGLPRPKSAGTATQWROSSSWTRVFQSWMDNLRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQWROSSSWTRVFQSWMDNLRGSSAPSQ 168

RESULT 4

US-09-375-257-2
; Sequence 2, Application US/09375257
; Patent No. 6504022
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.

APPLICANT: Oltersdorf, Tilman
 TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
 FILE REFERENCE: 480140.428D1
 CURRENT APPLICATION NUMBER: US/09/375,257
 CURRENT FILING DATE: 1999-08-16
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 168
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-375-257-2

Query Match 100.0%; Score 905; DB 4; Length 168;
 Best Local Similarity 100.0%; Pred. No. 6, 7e-86;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQIPEFPESEODSSAERGLGSPAGDPSGSGKHROAPGLMDASHQOQPTSSSH 60
 DB 1 MQIPEFPESEODSSAERGLGSPAGDPSGSGKHROAPGLMDASHQOQPTSSSH 60
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPPLMAAQRVGRRLRMSDE 120
 DB 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPPLMAAQRVGRRLRMSDE 120
 QY 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVQSWMDRLNGRSSAPSQ 168
 DB 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVQSWMDRLNGRSSAPSQ 168

RESULT 5
 US-08-665-617-2
 Sequence 2, Application US/08665617
 Patent No. 563316
 GENERAL INFORMATION:
 APPLICANT: Xudong, Yin
 TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,617
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: CL-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-617-2

Query Match 83.0%; Score 751; DB 1; Length 166;
 Best Local Similarity 84.0%; Pred. No. 5, 1e-70;
 Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 MQIPEFPESEODSSAERGLGSPAGDPSGSGKHROAPGLMDASHQOQPTSSSH 60
 DB 1 MQIPEFPESEODSSAERGLGSPAGDPSGSGKHROAPGLMDASHQOQPTSSSH 60
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPPLMAAQRVGRRLRMSDE 120
 DB 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPPLMAAQRVGRRLRMSDE 120

Matches 147; Conservative 3; Mismatches 9; Indels 16; Gaps 3;
 QY 1 MQIPEFPESEODSSAERGLGSPAGDPSGSGKHROAPGLMDASHQOQPTSSSH 60
 DB 1 MQIPEFPESEODSSAERGLGSPAGDPSGSGKHROAPGLMDASHQOQPTSSSH 60
 QY 54 OPTSSHHGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPPLMAAQRVGRRE 113
 DB 52 OPTSSHHGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPPLMAAQRVGRRE 111
 QY 114 LRMSDEPVDSFKKGLPRPKSAGTATQWRQSSSWTRVQSWMDRLNGRSSAPSQ 168
 DB 112 LRMSDEPVDSFKKGLPRPKSAGTATQWRQSSSWTRVQSWMDRLNGRSSAPSQ 166

RESULT 6
 US-08-985-335-7
 Sequence 7, Application US/08985335
 Patent No. 6080847
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preeti
 APPLICANT: Shah, Purni
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,335
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0421 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 1683637
 US-08-985-335-7

Query Match 82.2%; Score 744; DB 3; Length 168;
 Best Local Similarity 85.1%; Pred. No. 2, 7e-69;
 Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 MQIPEFPESEODSSAERGLGSPAGDPSGSGKHROAPGLMDASHQOQPTSSSH 60
 DB 1 MQIPEFPESEODSSAERGLGSPAGDPSGSGKHROAPGLMDASHQOQPTSSSH 60
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPPLMAAQRVGRRLRMSDE 120
 DB 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPFRGRSRAPPLMAAQRVGRRLRMSDE 120

Db 61 HGGWGCDDPSPOLLPRGDDGRRRDGGAGPFRGRSRAPPNLMAAQRYSRELRMSDE 120
Qy 121 FVDSFKKGLPRPKSAGTATKORSSSWTRVFGSWMDRNLGSGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATKORSSSWTRVFGSWMDRNLGSGSSAPSQ 168

RESULT 7

US-09-410-372-7
Sequence 7, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Cortley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-09-410-372-7

Query Match 82.2%; Score 744; DB 3; Length 168;
Best Local Similarity 85.1%; Pred. No. 2.7e-69;
Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MFOIPEFPESEODSSAERGLGSPAGDGPSSGKHHRAPGLLMDASHOQOPTSSSH 60
Db 1 MFOIPEFPESEODSSAERGLGSPAGDGPSSGKHHRAPGLLMDASHOQOPTSSSH 60
Qy 61 HGGAGAVEIRSRHSSYPAGTEDECGMEEPSPFRGRSSAPPNLMAAQRYSRELRMSDE 120
Db 61 HGGWGCDDPSPOLLPRGDDGRRRDGGAGPFRGRSRAPPNLMAAQRYSRELRMSDE 120
Qy 121 FVDSFKKGLPRPKSAGTATKORSSSWTRVFGSWMDRNLGSGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATKORSSSWTRVFGSWMDRNLGSGSSAPSQ 168

RESULT 8
US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Knourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note="Deduced amino acid sequence
of mouse BAD"
US-08-333-565-2

Query Match 71.7%; Score 649; DB 1; Length 204;
Best Local Similarity 75.6%; Pred. No. 2.2e-59;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

Qy 1 MFOIPEFPESEODSSAERGLGSPAGDGPSSGKHHRAPGLLMDASHOQOPTSSSH 60
Db 43 MFOIPEFPESEODSSAERGLGSPAGDGPSSGKHHRAPGLLMDASHOQOPTSSSH 97
Qy 61 HGGAGAVEIRSRHSSYPAGTEDECGMEEPSPFRGRSSAPPNLMAAQRYSRELRMSDE 120
Db 98 HGGAGAVEIRSRHSSYPAGTEDECGMEEPSPFRGRSSAPPNLMAAQRYSRELRMSDE 157
Qy 121 FVDSFKKGLPRPKSAGTATKORSSSWTRVFGSWMDRNLGSGSSAPSQ 168
Db 158 FEGGF-KGLPRPKSAGTATKORSSSWTRVFGSWMDRNLGSGSSAPSQ 204

RESULT 9
US-08-661-479-2
Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59

RESULT 10
US-08-733-505A-1
Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105

RESULT 11-
 US-08-733-505A-12
 : Sequence 12, Application US/08733505A
 : Patent No. 5856445
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: KORSMEYER, STANLEY J.
 : TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
 : TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
 : NUMBER OF SEQUENCES: 60
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: HOWELL & HARRKAMP, L.C.
 : STREET: 7733 FORSYTH BLVD., SUITE 1400
 : CITY: ST. LOUIS
 : STATE: MISSOURI
 : COUNTRY: USA
 : ZIP: 63105
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: FLOPPY disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/733,505A
 : FILING DATE:
 : CLASSIFICATION: 530
 : ATTORNEY/AGENT INFORMATION:
 : NAME: HOLLAND, DONALD R.
 : REGISTRATION NUMBER: 35,197
 : REFERENCE/DOCKET NUMBER: 965458
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (314) 727-5188

TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 4.5e-59;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFOIPEPESQEDSSAERGLGSPADGSPSGSKHROAAGLMDASHOQEPPTSSSH 60
DB 43 MFOIPEPESQEDSSAERGLGSPADGSPSGSKHROAAGLMDASHOQEPPTSSSH 97
QY 61 HGGAGAVEIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
DB 98 HGGAGAMETRSRHSYPAAGTEDEDEGMEELSPFRGRSRAPPNLMAAQRVGRRLRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFGSWMDRLNGSGSAPSQ 168
DB 158 FEGSF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWMDRLNGSGSTPSQ 204

RESULT 12
US-08-733-505A-13
Sequence 13, Application US/08733505A
Patent No. 5856445

GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
FAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 4.5e-59;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFOIPEPESQEDSSAERGLGSPADGSPSGSKHROAAGLMDASHOQEPPTSSSH 60

DB 43 MFOIPEPESQEDSSAERGLGSPADGSPSGSKHROAAGLMDASHOQEPPTSSSH 97
QY 61 HGGAGAVEIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
DB 98 HGGAGAMETRSRHSYPAAGTEDEDEGMEELSPFRGRSRAPPNLMAAQRVGRRLRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFGSWMDRLNGSGSAPSQ 168
DB 158 FEGSF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWMDRLNGSGSTPSQ 204

RESULT 13
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703

GENERAL INFORMATION:
APPLICANT: Horne, William A.
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
FAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-717-123-3

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 4.5e-59;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFOIPEPESQEDSSAERGLGSPADGSPSGSKHROAAGLMDASHOQEPPTSSSH 60
DB 43 MFOIPEPESQEDSSAERGLGSPADGSPSGSKHROAAGLMDASHOQEPPTSSSH 97
QY 61 HGGAGAVEIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
DB 98 HGGAGAMETRSRHSYPAAGTEDEDEGMEELSPFRGRSRAPPNLMAAQRVGRRLRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFGSWMDRLNGSGSAPSQ 168
DB 158 FEGSF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWMDRLNGSGSTPSQ 204

RESULT 14
US-09-375-257-3
Sequence 3, Application US/09375257
Patent No. 6504022


```

; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilmann
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D1
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-375-257-3

Query Match      71.4%; Score 646; DB 4; Length 204;
Best Local Similarity 75.0%; Pred. No. 4.5e-59;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGPPAGDPSGSGKHROAPGLMDASHQOEQPTSSSH 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 43 MFQIPFEPSEQEDSADTRGIGLPSLTEDQF---GPY--LAPGLGSHHQGRATNSH 97
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 HCGAGAVEIRSRHSSYPAGTEDEDEGMGEPSFPRGRSRAPPNLMAAORYGRELRRMSDE 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 98 HCGAGAMETRSRHSYVPAETEDDEGMGEELSFPGRSRAPPNLMAAORYGRELRRMTDE 157
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLRGSSAPSQ 168
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 158 FEGSF-KGLPRPKSAGTATQMRQSGWTRIIQSWMDRNLRGKGSTPSQ 204
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 15

```

US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-14

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Query Match      71.0%; Score 643; DB 2; Length 204;
Best Local Similarity 74.4%; Pred. No. 9.3e-59;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGPPAGDPSGSGKHROAPGLMDASHQOEQPTSSSH 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 43 MFQIPFEPSEQEDSADTRGIGLPSLTEDQF---GPY--LAPGLGSHHQGRATNSH 97
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 HCGAGAVEIRSRHSSYPAGTEDEDEGMGEPSFPRGRSRAPPNLMAAORYGRELRRMSDE 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 98 HCGAGAMETRSRHSYVPAETEDDEGMGEELSFPGRSRAPPNLMAAORYGRELRRMSDE 157
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLRGSSAPSQ 168
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 158 FEGSF-KGLPRPKSAGTATQMRQSGWTRIIQSWMDRNLRGKGSTPSQ 204
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: December 29, 2003, 23:36:13
Job time : 31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003. Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 22:58:29 ; Search time 37 Seconds
(without alignments)
436.658 Million cell updates/sec

Title: US-10-066-179-2

Perfect score: 905
Sequence: 1 MFQIPEFPESSQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	71.7	204	A55671	bad protein - mouse
2	95	10.5	834	T42702	hypothetical prote
3	93.5	10.3	1729	T18396	erythrocyte membra
4	93	10.3	1300	T03166	probable immediate
5	92.5	10.2	336	T30757	hypothetical prote
6	91.5	10.1	2248	A35938	profilaggrin - hum
7	90	9.9	646	S15901	chromogranin B pre
8	90	9.9	2237	T45115	N-type calcium cha
9	90	9.9	2339	A42566	omega-conotoxin-se
10	89.5	9.9	449	A41520	chromogranin A pre
11	88.5	9.8	393	JC5614	RNB6 protein - rat
12	86.5	9.6	1077	A44067	serine-rich protei
13	86.5	9.6	1647	S45252	SNFbeta protein -
14	86.5	9.6	2715	T13049	eyelid - fruit fly
15	86	9.5	222	T43500	hypothetical prote
16	86	9.5	270	WJMS13	homeotic protein H
17	86	9.5	343	T05221	hypothetical prote
18	86	9.5	420	B38104	LFY floral meriste
19	85.5	9.4	254	A31488	filaggrin - mouse
20	85	9.4	337	T49431	endoenzyme related
21	85	9.4	380	SS1797	vasodilator-stimul
22	85	9.4	1095	T200329	hypothetical prote
23	84.5	9.3	134	T54810	PHL ELF1 - human
24	84.5	9.3	380	T24786	hypothetical prote
25	84.5	9.3	1159	T13845	probable potassium
26	84.5	9.3	1323	T00037	hypothetical prote
27	84.5	9.3	1562	T29146	hypothetical prote
28	84	9.3	270	WHNUIC	homeotic protein H
29	84	9.3	313	A28444	filaggrin precursor

30	84	9.3	381	2	S16506	hypothetical prote
31	84	9.3	542	2	A44358	zyxin - chicken
32	84	9.3	886	2	S07132	hypothetical prote
33	84	9.3	2023	2	T13154	polycarb protein e
34	83.5	9.2	625	2	A34615	profilaggrin - rat
35	83.5	9.2	672	2	T40333	tracheal colonizat
36	83.5	9.2	1215	2	T32734	myosin-1A - Acanth
37	83.5	9.2	1392	2	T51947	probable transcrip
38	83.5	9.2	3759	2	A35085	trithorax protein
39	83	9.2	263	1	EB08A	enkephalin e-12 pr
40	83	9.2	743	2	T09173	EH domain protein
41	83	9.2	760	2	T16726	hypothetical prote
42	82.5	9.1	523	2	T36677	probable secretory
43	82.5	9.1	558	2	A33616	heterogeneous ribo
44	82.5	9.1	635	2	T09648	nucleolin homolog
45	82.5	9.1	751	2	T02858	hypothetical prote

ALIGNMENTS

RESULT 1

A55671
bad protein - mouse
C.Species: Mus musculus (house mouse)
C.Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C.Accession: A55671
R.Yang, E., Zha, J., Jockel, J., Boise, L.H., Thompson, C.B., Korsmeyer, S.J.
Cell 80, 285-291, 1995
A>Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promotes
A.Reference number: A55671; MUID:95136361; PMID:7834748
A.Accession: A55671
A>Status: preliminary; not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-204 <YAN>
A.Cross-references: GB:LJ7296; NID:G639778; PIDN:AAA64465.1; PID:G639779
C.Keywords: heterodimer

Query Match 71.7%; Score 649; DB 2; Length 204;
Best Local Similarity 75.6%; Pred. No. 2.7e-45;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY	1	MFQIPEFPESSQEDSSAERGLGPSAGDGPSSGSKHROAPGLMDASHOQEOPTSSSH	60
DB	43	MFQIPEFPESSQEDASATDRGLGPSLTEDQ---GPV--LAPGLGSYTHQCGRAATSH	97
QY	61	HGAGAVEIRSRSSYPAGTEDEMGCEPSPFRGRSRAPPNLMAAQRVRELRMSDE	120
DB	98	HGAGAMETRSRSHSSYPAGTEDEMGCEBELSPFRGRSRAPPNLMAAQRVRELRMSDE	157
QY	121	FVDSFKTKGLPRPKSAGTATQROSSSWTRVQSWMDRLGRGSSAPSQ	168
DB	158	FEQSF-KGLPRPKSAGTATQROSGAGWTRIIQSWMDRLGRGSGTSPSQ	204

RESULT 2

T42702
hypothetical protein DKFZp434F117.1 - human (fragment)
N.Alternate names: hypothetical protein DKFZp434B239.1
C.Species: Homo sapiens (man)
C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Jun-2000
C.Accession: T42702; T46502
R.Kocher, K., Beyer, A., Mewes, H.W., Gassenhuber, J., Wiemann, S.
Submitted to the Protein Sequence Database, November 1999
A.Reference number: 222234
A.Accession: T42702
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-834 <AAA>
A.Cross-references: EMBL:AL133028
A.Experimental source: adult testis; clone DKFZp434F117
R.Pouska, A., Klein, M., Mewes, H.W., Gassenhuber, J., Wiemann, S.
Submitted to the Protein Sequence Database, January 2000

A:Reference number: A35938; MUID:91064347; PMID:2248957
 A:Accession: A35938
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-2248 <GAN>
 A:Cross-references: GB:J02929
 C:Genetics:
 A:Gene: GDB:FLG
 A:Cross-references: GDB:119912; OMIM:135940
 A:Map position: 1q21-1q21
 C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology
 C:Keywords: BF hand; epidermis; polymorphism; tandem repeat
 F:1246-569/Region: filaggrin repeat
 F:570-893/Region: filaggrin repeat
 F:1074-1397/Region: filaggrin repeat
 F:1573-1896/Region: filaggrin repeat

Query Match 10.1%; Score 91.5; DB 2; Length 2248;
 Best Local Similarity 28.1%; Pred. No. 25;
 Matches 41; Conservative 15; Mismatches 55; Indels 35; Gaps 5;

QY 11 EEDSSAER-GLGPPADGPGSGGKHROAPGLMDASHQEQPTSSHHG----- 63
 DB 152 EQRRSAGRHGSHHQQSDSSRHSGTGHQASTAVSDGHRGYSQASDNEGHSESD 211
 QY 64 ---AGAVEIRSHSSYPAGTEDEMGCEPSPFGRSRAPNLMAORYGELRMGD 119
 DB 212 SQSVAGQRRARSHHQHST-----RRSRG-----GSRGSRFLYQVST 252

QY 120 EFVDSFKGLPRPKSAGTATQMRQS 145
 DB 253 HQSSSHGWAR-----TSTGRQGS 273

RESULT 7
 S15901
 Chromogranin B precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: S15901; S20727; A61076; S21773; S93369
 R:Bauer, J.W.; Fischer-Colbride, R.
 Biochem. Biophys. Acta 1089, 124-126, 1991
 A:Title: Primary structure of bovine chromogranin B deduced from cDNA sequence.
 A:Reference number: S15901; MUID:91223091; PMID:2025642
 A:Accession: S15901
 A:Molecule type: mRNA
 A:Residues: 1-646 <BIO>
 A:Cross-references: EMBL:X55027; NID:g11; PIDN:CAA3846.1; PID:g12
 R:Grandy, D.K.; Leduc, R.; Makam, H.; Flanagan, T.; Diliberto, E.J.; Thomas, G.; Civeili
 submitted to the EMBL Data Library, October 1990
 A:Description: Nucleotide and deduced amino acid sequence of bovine adrenal medulla chro
 A:Reference number: S20727
 A:Accession: S20727
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 21-63; 'N', 65-92, 'FRS', 96, 'RA', 99-100, 'S', 101-480, 'L', 482-646 <GRA>
 A:Cross-references: EMBL:X55489; NID:g201; PIDN:CAA33109.1; PID:g202
 R:Flanagan, T.; Taylor, L.; Poulier, L.; Viveros, O.H.; Diliberto Jr., E.J.
 Cell. Mol. Neurobiol. 10, 507-523, 1990
 A:Title: A novel 1745-Dalton pyroglutamate1 peptide derived from chromogranin B is in the
 A:Reference number: A61076; MUID:91223542; PMID:1982622
 A:Accession: A61076
 A:Molecule type: protein
 A:Residues: 567-580 <FLA>
 R:Dillen, L.; Boel, S.; de Potter, W.P.; Claeys, M.
 Biochim. Biophys. Acta 1120, 105-112, 1992
 A:Title: Mass spectrometric characterization of bovine chromaffin granule peptides relat
 A:Reference number: S21773; MUID:92207983; PMID:1554736
 A:Accession: S21773
 A:Molecule type: protein
 A:Residues: 567-580 <DL>
 R:Yoo, S.H.
 Biochim. Biophys. Acta 1179, 239-246, 1993

A:Title: pH-dependent binding of chromogranin B and secretory vesicle matrix proteins to
 A:Reference number: S39369; MUID:94032431; PMID:8218367
 A:Accession: S39369
 A:Molecule type: protein
 A:Residues: 239-244; 562-565 <YOO>
 A:Superfamily: chromogranin B precursor
 C:Keywords: adrenal gland; glycoprotein; pituitary; pyroglutamic acid; sulfoprotein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-646/Product: chromogranin B #status predicted <MAT>
 F:567-580/Product: pyroglutamy1 peptide BAW-1745 #status experimental <MA2>
 F:136-57/Disulfide bonds: #status predicted
 F:188/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:315/Binding site: sulfate (tyr) (covalent) #status predicted
 F:567/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime

Query Match 9.9%; Score 90; DB 1; Length 646;
 Best Local Similarity 28.7%; Pred. No. 87;
 Matches 37; Conservative 16; Mismatches 53; Indels 24; Gaps 6;

QY 9 PEOEDSSAERGLGPPADGPGSGGKH--RQAPGLMDASHQEQP--TSSHHGCA 64
 DB 246 PGESEDA-----SFVDKRHSPRHHRSP-----DRSSQGNPRLBESHVGTG 293

QY 65 GAVEIRSHSSYPAGTEDEMGCEPSPFGRSRAPNLMAORYGR-----ELRMS 118
 DB 294 NDEKKAHPHAFRLAECAEYGEVR--RHSAAQPDQLQAFRGGRGHEHQLRPS 351

QY 119 DEFVDSFK 127
 DB 352 EESLEQENK 360

RESULT 8
 T45115
 N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 A:Accession: T45115
 R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patch, S.; Simerson, S.; Maroufi, A.; McC
 Science 257, 389-395, 1992
 A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
 A:Reference number: A42566; MUID:92335886; PMID:1321501
 A:Accession: T45115
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2237 <WIL>
 A:Cross-references: EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PID:g179760
 A:Experimental source: cell line IMR32; neuroblastoma
 A:Genetics:
 A>Note: CCH1A2
 C:Function: calcium influx
 A:Description: voltage-dependent calcium channel protein alpha-1 chain
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 9.9%; Score 90; DB 2; Length 2237;
 Best Local Similarity 30.8%; Pred. No. 33;
 Matches 36; Conservative 16; Mismatches 35; Indels 30; Gaps 9;

QY 8 EPEQED-----SSAERGLGPPA-----GDGPGSGGKHROAPGLMDA----- 48
 DB 878 EFGAEEPRPHRHSKCAAPPEARSRGPGEGRRHRR--GSPBEAAREPRRH 935

QY 49 -SHQEQPTSSHHGGAANV-EIISRHSYP-AGTEDEMGCEPSPFGRSRAP 101
 DB 936 RAHRQDPSKCC---AGAKGERRRARRHGPRAGPRAES--GEPARRRRARRHQAQ 987

RESULT 9
 A42566
 omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively splic
 C:Species: Homo sapiens (man)
 C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
 A:Accession: A42566

R;Williams, M.E.; Brunet, P.F.; Feldman, D.H.; Patti, S.; Simerson, S.; Maroufi, A.; McScience 257, 389-395, 1992
 A>Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
 A:Reference number: A42566; MUID:92335886; PMID:1321501
 A:Accession: A42566
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-2339 <WTL>
 A:Experimental source: IMR32, hippocampus
 A>Note: sequence extracted from NCBI backbone (NCBI:109168)
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 9.9%; Score 90; DB 2; Length 2339;
 Best Local Similarity 30.8%; Pred. No. 35;
 Matches 36; Conservative 16; Mismatches 35; Indels 30; Gaps 9;

Qy 8 EPSEGED-----SSSAERGLGPSA-----GDGSGSGKHHKQAPGLMVA----- 48
 Db 878 EPQAEERPRPRHSKFAAGPEPARSERGPGEGRRHRR--GSPEEAEREPRRH 935

Qy 49 -SHQOEPTSSSHHGAGAV-EIRSRHSYP-AGTEDEMGGEPS-PPGRSRAP 101
 Db 936 RAHRHQDSKXC---AKAKERRRRHRRGPRAGREMS-GEPRARRRRHAKQ 987

RESULT 10
 A41520
 chromogranin A precursor [validated] - bovine
 N:Alternate names: pituitary secretory protein I; secretory protein I
 N:Contains: chromostatin; pancreastatin
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 18-Aug-2000
 R:Accession: A41520; A28033; A24175; A60306; A61114; S15847; S39016; I46008; S38976
 R:Accession: A41520; A28033; A24175; A60306; A61114; S15847; S39016; I46008; S38976
 Mol. Endocrinol. 5, 1651-1660, 1991
 A>Title: The bovine chromogranin A gene: structural basis for hormone regulation and gen
 A:Reference number: A41520; MUID:92140395; PMID:1779968
 A:Accession: A41520
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-449 <IAC>
 A:Cross-references: GB:S79270; NID:g244423; PIDN:AA21297.1; PID:g244424
 R:Alm, T.G.; Cohn, D.V.; Gorr, S.U.; Onstiein, D.L.; Kashdan, M.A.; Levine, M.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5043-5047, 1987
 A>Title: Primary structure of bovine pituitary secretory protein I (chromogranin A) deduc
 A:Reference number: A28033; MUID:87260925; PMID:3474638
 A:Accession: A28033
 A:Molecule type: mRNA
 A:Residues: 1-111, 'T', 113-190, 'Y', 192-253, 'P', 255-378, 'R', 380-449 <AHN>
 A:Cross-references: GB:M16971; NID:g163727; PIDN:AA30765.1; PID:g163728
 R:Note: the authors translated the codon CCG for residue 391 as Gln
 R:Accession: A41520; A28033; A24175; A60306; A61114; S15847; S39016; I46008; S38976
 Nature 323, 82-86, 1986
 A>Title: Bovine chromogranin A sequence and distribution of its messenger RNA in endocr
 A:Reference number: A24175; MUID:86311345; PMID:3018587
 A:Accession: A24175
 A:Molecule type: mRNA
 A:Residues: 1-153, 'P', 156-158, 'R', 160-190, 'Y', 192-253, 'P', 255-449 <IA2>
 A:Cross-references: GB:X04298; NID:g217; PIDN:CAA27841.1; PID:g218
 R:Nakano, I.; Funakoshi, A.; Miyasaka, K.; Ishida, K.; Maki, G.; Angwin, P.; Chang, D.;
 Regul. Pept. 25, 207-213, 1989
 A>Title: Isolation and characterization of bovine pancreastatin.
 A:Reference number: A60306; MUID:89331945; PMID:2756155
 A:Accession: A60306
 A:Molecule type: protein
 A:Residues: 266-312 <NAK>
 R:Barbosa, J.A.; Gill, B.M.; Takiiyuddin, M.A.; O'Connor, D.T.
 Endocrinology 128, 174-190, 1991
 A>Title: Chromogranin A: posttranslational modifications in secretory granules.
 A:Reference number: A61114; MUID:91099142; PMID:1986917
 A:Accession: A61114
 A:Molecule type: protein
 A:Residues: 19-34, 'X', 36-38, 97-111, 134-139 <BA2>

R;Watkinson, A.; Joensen, A.C.; Davison, M.; Young, J.; Lee, C.M.; Moore, S.; Dockray, C
 Biochem. J. 276, 471-479, 1991
 A>Title: Heterogeneity of chromogranin A-derived peptides in bovine gut, pancreas and ad
 A:Reference number: S15847; MUID:91264803; PMID:1710890
 A:Accession: S15847
 A:Molecule type: protein
 A:Residues: 266-310, 'H', 312-318, 'K', 320-331 <WA2>
 A>Note: 311-Arg and 319-Glu were also found
 R;Watkinson, A.; Rogers, M.; Dockray, G.J.
 Biochem. J. 295, 649-654, 1993
 A>Title: Post-translational processing of chromogranin A: differential distribution of p
 A:Reference number: S39016; MUID:94039013; PMID:8240272
 A:Accession: S39016
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 303-331 <WAT>
 R:Benedum, U.M.; Baueerle, P.A.; Konecki, D.S.; Frank, R.; Powell, J.; Hutter
 EMBO J. 5, 1495-1502, 1986
 A>Title: The primary structure of bovine chromogranin A: a representative of a class of
 A:Reference number: I46008; MUID:86300648; PMID:3755681
 A:Accession: I46008
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-135, 'S', 137-190, 'Y', 192-253, 'P', 255-310, 'H', 312-318, 'K', 320-390, 'Q', 392-445
 A:Cross-references: EMBL:X04012; NID:9197; PIDN:CAA27636.1; PID:g198
 R:Yoo, S.H.; Ferretti, J.A.
 FEBS Lett. 334, 373-377, 1993
 A>Title: Nature of the pH-induced conformational changes and exposure of the C-terminal
 A:Reference number: S38976; MUID:94063061; PMID:8243650
 A:Accession: S38976
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 19-26, 266-272 <YOO>
 C:Comment: Chromogranin A is the major protein of bovine chromagrin granules.
 C:Comment: Chromostatin activity has been demonstrated from proteolytic fragments of chr
 C:Genetics: 16/1; 31/3; 63/1; 86/1; 119/1; 266/1; 422/3
 A:Introns: 16/1; 31/3; 63/1; 86/1; 119/1; 266/1; 422/3
 C:Superfamily: chromogranin A
 C:Keywords: phosphoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-449/Product: chromogranin A #status experimental <MAT>
 F:142-161/Product: chromostatin #status predicted <MAT3>
 F:266-312/Product: pancreastatin #status experimental <MAT2>
 F:35-56/Duplicate bonds: #status predicted

Query Match 9.9%; Score 89.5; DB 1; Length 449;
 Best Local Similarity 24.4%; Pred. No. 6.4;
 Matches 39; Conservative 19; Mismatches 57; Indels 45; Gaps 8;

Qy 6 EFPSBOE---DSSAERGLGPSAGDPGSGGKHHKQAPGLMDASHQOEPTSSSHG 62
 Db 138 EFKSDSDSDODRQAQAPGLGPGP-----KVEDNQAGP-----EEEAAPSNAH-- 181

Qy 63 GAGAVEIRSRHSSTPATTEDEMGGEPSPPGRGSRAPVLMVAQYGEILRMSP-- 119
 Db 182 --PLASPPSPHPGPAKEDSEGPSQPA-----SREKGLSAEO--GRQTEREEEEK 230

Qy 120 -EPVDSFKKGLPR-----PKSAGTATQWRQSSW 147
 Db 231 WEBAAREKAVPESEPTTAFAKAPSLGNKKTORAAPGM 270

RESULT 11
 JC5614
 RN66 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 23-Sep-1997 #sequence revision 17-Oct-1997 #text change 05-Nov-1999
 C:Accession: JC5614
 R:Ohba, S.; Mineita, T.; Kimoto, M.; Tabuchi, K.
 Biochem. Biophys. Res. Commun. 237, 307-312, 1997
 A>Title: Differential display cloning of a novel rat cDNA (RN66) that shows high express
 A:Reference number: JC5614; MUID:97415794; PMID:9268706
 A:Accession: JC5614

A/Molecule type: mRNA
A:Residues: 1-393 <OHT>
A:Cross-references: GB:U70211; NID:g2058461; PIDN:AAC53322.1; PID:g2058462
A:Experimental source: brain
C:Comment: This protein belongs to Ena/VASP family member, and is involved in the development.

Query Match 9.6%; Score 86.5; DB 2; Length 393;
Best Local Similarity 28.2%; Pred. No. 6.7;
Matches 40; Conservative 16; Mismatches 45; Indels 41; Gaps 7;

QY 13 EDSASAEKGLGSPADGSGGSKHHRQAPGLMDASHOQEOPTSSHHGAGAVEIRSR 72
DB 237 EDAS-----GGSSPSGTSKS-----DANR-----ASSGGGGGGLMEENMK 271

QY 73 -----HSSYPAGTDEDEGMBEP--SPPRG-RSRSAAPPNMAAQRGRELARMSD 119
DB 272 LLAQRKAASQTDKPEADKEDENQTDPTSPSGSRATSPQPNSSSEAGKPKWERNISVE 331

QY 120 EFVDSFKKGLPRPKSAGTATQM 141
DB 332 KPVSSL---LSRVKPKAGSYNDV 350

RESULT 12
A44067
serine-rich protein hairless - fruit fly (Drosophila melanogaster)
N:Alternate names: 109k basic protein H
C:Species: Drosophila melanogaster
C>Date: 10-Jun-1993 #sequence_revision 26-Feb-1999 #text_change 26-Feb-1999
C:Accession: A44067; A58929; S33412; S24639
R:Bang, A.G.; Posakony, J.W.
Gene Dev. 6, 1752-1769, 1992

A:Title: The Drosophila gene Hairless encodes a novel basic protein that controls altert
A:Reference number: A44067; MUID:92387549; PMID:1516831
A:Accession: A44067
A:Molecule type: DNA

A:Residues: 19-1077 <BAN>
A:Cross-references: GB:M95192; NID:G157621; PID:G157622
A:Note: sequence extracted from NCBI backbone (NCBIN:112622, NCBIPI:112623)
R:Preiss, A.
Submitted to the EMBL Data Library, May 1994

A:Description: Hairless, a Drosophila gene involved in neural development, encodes a nov
A:Reference number: A58929
A:Accession: A58929
A:Molecule type: mRNA

A:Residues: 1-1077 <PRB>
A:Cross-references: EMBL:X67239; GB:S49642; NID:G578331; PID:G578332
R:Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.
Mech. Dev. 38, 143-156, 1992

A:Title: Hairless, a Drosophila gene involved in neural development, encodes a novel, se
A:Reference number: S33412; MUID:93041287; PMID:1419850
A:Accession: S33412
A:Molecule type: mRNA

A:Residues: 1-150, 'A', 152-701, 'LV', 704-890, 'R', 892-963, 'RLP', 968-973, 975-1077 <MAI>
A:Cross-references: EMBL:X67239
C:Genetics:

A:Gene: FlyBase:H; hairless
A:Cross-references: FlyBase:FBgn0001169

Query Match 9.6%; Score 86.5; DB 2; Length 1077;
Best Local Similarity 28.9%; Pred. No. 29;
Matches 37; Conservative 17; Mismatches 47; Indels 27; Gaps 7;

QY 15 SSSARGLGSPAGCPSC--SGKHHQAPGLMDASHOQEOPTSSHHGAGAVEIRSR 72
DB 678 SSSSSSG--KKCGHPAIIISNVHPQ-----HSMYPPSSSSYPRAL---LNSP 721

QY 73 HSSYPAGTDEDEGMBEPSPPRGSRSAAPPNMAAQRGRELARMSEFVDSFKKGLRPP 132
DB 722 KSPDVSGS--NCGGKSPSHGTGKRSPPYSAGSPVDYGHSHYR--DPYA-----GAGR 772

QY 133 KSAGTATQ 140

DB 773 STGSASQ 780

RESULT 13
S45252

SNFbeta protein - human
C:Species: Homo sapiens (man)
C>Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 02-Aug-2002
C:Accession: S45252
R:Chida, H.; Muramatsu, M.; Nomoto, A.; Kato, H.
Nucleic Acids Res. 22, 1815-1820, 1994
A:Title: Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and Drosophila brah

A:Reference number: S45251; MUID:94268902; PMID:820605
A:Accession: S45252
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-1647 <CHI>
A:Cross-references: GB:D26156; NID:g505087; PIDN:BAA05143.1; PID:g505088
C:Superfamily: human SNF2alpha protein; bromodomain homology
F:1485-1540/Domain: bromodomain homology <BRO>

Query Match 9.6%; Score 86.5; DB 2; Length 1647;
Best Local Similarity 29.8%; Pred. No. 46;
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;

QY 9 PSEQDSSAEKGLGSPAGCPSCGSKH--RQAP-GLMDASHOQEOPTSSHHGCA 64
DB 30 PSPGSPGSAHSMWSPSP--GPPSAG--HPIPTGPGGYPDNNHQMHPMESHEKGM 84

QY 65 GAVEIRSHSSYPAGTDEDEGMBEPSPPRGSRSAAPPNMAAQ 108
DB 85 SDDPRYNNQMKGMKMGSRSGHAGMGPPSPMDHSGQYBPPLGSS 128

RESULT 14
T13049

eyelid - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
R:Trelsmann, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
Submitted to the EMBL Data Library, March 1998

A:Reference number: Z17592
A:Accession: T13049

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA
A:Residues: 1-2715 <TRB>

A:Cross-references: EMBL:AF053091; NID:g2981220; PID:g2981221; PIDN:AAC06254.1
C:Genetics:

A:Gene: eld
A:Cross-references: FlyBase:FBgn0003013
C:Function:

A:Description: could act as a transcription factor antagonistic to the Wg pathway
C:Keywords: DNA binding

Query Match 9.6%; Score 86.5; DB 2; Length 2715;
Best Local Similarity 25.8%; Pred. No. 79;
Matches 41; Conservative 11; Mismatches 48; Indels 59; Gaps 10;

QY 8 EPSEQDSSAEKGLG-PSPADGSPSGSKHHRQAPG-----LLMDASHOQEOPTSSHHGCA 55
DB 54 DPSTIQOQNVAPRPGAPPPGSGPBG-----PFGDPAVAVHTYHNLHQOQOQHPPPP 106

QY 56 -TSSSHHGAGAVEIRSHSSYPAGT-EDDEGMBEP-----PSPFRGRSRGAPPNL 104
DB 107 HMQOQHNGGAPAPP-----PGAGPBNAPGVGVEYTHLPHPHPAYGRYH-ADBNM 157

QY 105 WAAQRGRELARMSEFVDSFKKGLPRPKSAGTATQM 143
DB 158 -----DPRYGOPLP--GKPPQOQO 176

RESULT 15

T43500

hypothetical protein DKFZp586G1721.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C;Accession: T43500

R;Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, December 1999

A;Reference number: Z22515

A;Accession: T43500

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-222 <AAA>

A;Cross-references: EMBL:AL133642

A;Experimental source: adult uterus; clone DKFZp586G1721

C;Genetics:

A;Note: DKFZp586G1721.1

Query Match 9.5%; Score 86; DB 2; Length 222;

Best Local Similarity 27.3%; Pred. No. 5.7; 56; Indels 38; Gaps 6;

Matches 41; Conservative 15; Mismatches 56; Indels 38; Gaps 6;

QY 13 EDSSSAERGLGPSPAGDGPSSGKHHQAPGLMDASHQOQPTSSHHGAGAVETRSR 72

Db 77 EDAS-----GGSSPSGTSKS-----DANR-----ASGGGGGGLMEENK 111

QY 73 -----HSSYPAGTDEDEGMGEPP--SPFRG-RSRSA-PNULMAQRYGRELRRMSD 119

Db 112 LLAARRKAASQSDKPAEKEDSOMEDPSTSPSTRASQPPNSSEAGRKWERNSVE 171

QY 120 EFVDSFKKGLPRPKSAGTATQWRQSSSWTR 149

Db 172 KPVSSILSRTPSVAKSPKASPLQSQPHSR 201

Search completed: December 29, 2003, 23:35:33

Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 23:34:49 ; Search time 70 Seconds
(without alignments)
477.642 Million cell updates/sec

Title: US-10-066-179-2

Perfect score: 905
Sequence: 1 MFQIPEFPESEGEEDSSAER.....RVFQSWMDNLGRGSAPEQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications AA.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	905	100.0	168	9	US-09-922-378-2
2	905	100.0	168	9	US-09-894-657-1
3	905	100.0	168	12	US-10-209-967-2
4	905	100.0	168	14	US-10-066-179-2
5	744	82.2	168	9	US-09-894-657-7
6	649	71.7	204	12	US-10-209-967-4
7	646	71.4	204	9	US-09-922-378-3
8	646	71.4	204	14	US-10-066-179-3
9	132	14.6	25	15	US-10-059-261-258
10	95.5	10.6	923	11	US-09-820-843A-112
11	93.5	10.3	515	15	US-10-071-838-6
12	93.5	10.3	549	12	US-10-094-466-62
13	93.5	10.3	549	15	US-10-071-838-2
14	93.5	10.3	549	15	US-10-071-838-18
15	93.5	10.3	610	15	US-10-071-838-4

16	92.5	10.2	1402	12	US-10-379-616-12	Sequence 12, Appl
17	92	10.2	312	15	US-10-156-761-10983	Sequence 10983, A
18	91.5	10.1	845	15	US-10-174-677-32	Sequence 32, Appl
19	91	10.1	428	15	US-10-091-438-155	Sequence 155, App
20	91	10.1	430	9	US-09-764-853-564	Sequence 564, App
21	90.5	10.0	1101	15	US-10-174-363-54	Sequence 54, Appl
22	90	9.9	2237	14	US-10-033-026-8	Sequence 8, Appl
23	90	9.9	2339	14	US-10-033-026-6	Sequence 6, Appl
24	90	9.9	2343	14	US-10-033-026-4	Sequence 4, Appl
25	89	9.8	17	15	US-10-174-105A-136	Sequence 136, App
26	88.5	9.8	393	9	US-09-823-240-11	Sequence 11, Appl
27	87	9.6	418	15	US-10-177-293-401	Sequence 401, App
28	87	9.6	456	10	US-09-764-868-985	Sequence 985, App
29	86.5	9.6	245	8	US-08-424-550B-19	Sequence 39, Appl
30	86.5	9.6	735	15	US-10-128-714-1040	Sequence 3040, Ap
31	86.5	9.6	842	15	US-10-128-714-8040	Sequence 8040, Ap
32	86.5	9.6	1647	11	US-09-824-574-4	Sequence 4, Appl
33	86	9.5	386	15	US-10-177-293-403	Sequence 403, App
34	86	9.5	588	12	US-10-134-102-1	Sequence 1, Appl
35	86	9.5	591	11	US-09-291-417-103	Sequence 103, App
36	86	9.5	591	12	US-10-134-102-4	Sequence 4, Appl
37	86	9.5	591	12	US-10-394-332A-48	Sequence 48, Appl
38	85	9.4	380	9	US-09-823-240-10	Sequence 10, Appl
39	85	9.4	380	12	US-10-311-093-1	Sequence 1, Appl
40	85	9.4	635	15	US-10-072-036-125	Sequence 125, App
41	85	9.4	1554	12	US-10-301-822-93	Sequence 93, Appl
42	84.5	9.3	354	12	US-10-369-493-16044	Sequence 16044, A
43	84.5	9.3	841	12	US-10-332-795-11	Sequence 11, Appl
44	84.5	9.3	1065	15	US-10-174-363-28	Sequence 28, Appl
45	84.5	9.3	1097	12	US-10-288-798-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-922-378-2
; Sequence 2, Application US/09922378
; Patent No. US20020037869A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-378-2

Query Match 100.0% Score 905; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 6.9e-71;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFQIPEFPESEGEEDSSAERGLGPGSPADGSGSGKHHROAAGLMDASHQOEPTSSSH	60
DB	1	MFQIPEFPESEGEEDSSAERGLGPGSPADGSGSGKHHROAAGLMDASHQOEPTSSSH	60
QY	61	HGAGAVIRSHSHYPACTDEDEMGEBSPFGRSSAPPNLMAAORYGELRMSDE	120
DB	61	HGAGAVIRSHSHYPACTDEDEMGEBSPFGRSSAPPNLMAAORYGELRMSDE	120
QY	121	FVDSFKKGLPRPKSAGTATOWKROSSWTRVQSWMDNLGRGSSAPSQ	168
DB	121	FVDSFKKGLPRPKSAGTATOWKROSSWTRVQSWMDNLGRGSSAPSQ	168

RESULT 2

US-09-894-657-1
; Sequence 1, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Inventor: Hillman, Jennifer L.
; Inventor: Lal, Preeti
; Inventor: Shah, Purvi
; Inventor: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/894,657
; FILING DATE: 28-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/410,372
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-894-657-1
; Query Match 100.0%; Score 905; DB 9; Length 168;
; Best Local Similarity 100.0%; Pred. No. 6,9e-71;
; Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Db 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSSGSKHROAPGLMDASHQOEPITSSSH 60
; 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSSGSKHROAPGLMDASHQOEPITSSSH 60
; Db 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; Db 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; RESULT 3
; US-10-209-967-2
; Sequence 2, Application US/10209967
; Publication No. US20030171279A1
; GENERAL INFORMATION:
; APPLICANT: MÜNGER, JOSHUA
; APPLICANT: ROIZMAN, BERNARD

check
if ok

; TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
; FILE REFERENCE: ARCD-380US
; CURRENT APPLICATION NUMBER: US/10/209,967
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 60/308,929
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Human BAD
; US-10-209-967-2
; Query Match 100.0%; Score 905; DB 12; Length 168;
; Best Local Similarity 100.0%; Pred. No. 6,9e-71;
; Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Db 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSSGSKHROAPGLMDASHQOEPITSSSH 60
; 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSSGSKHROAPGLMDASHQOEPITSSSH 60
; Db 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; Db 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; RESULT 4
; US-10-066-179-2
; Sequence 2, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilmann
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140,428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-066-179-2
; Query Match 100.0%; Score 905; DB 14; Length 168;
; Best Local Similarity 100.0%; Pred. No. 6,9e-71;
; Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Db 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSSGSKHROAPGLMDASHQOEPITSSSH 60
; 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSSGSKHROAPGLMDASHQOEPITSSSH 60
; Db 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; Db 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; 61 HGGAGAVIRSRHSSYPAGTEDEDEGMEEPSPFRGRSRAPPNLMAAQRVGRRLRMSDE 120
; Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
; RESULT 5
; US-09-894-657-7
; Sequence 7, Application US/09894657
; Patent No. US20020098569A1

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Yue, Henry
Lal, Preeti
Shah, Puri
Cortley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1683637
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-894-657-7

Query Match 82.2%; Score 744; DB 9; Length 168;
Best Local Similarity 85.1%; Pred. No. 6.1e-57;
Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHROAQLMDASHOQEOPTSSSH 60
DB 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHROAQLMDASHOQEOPTSSSH 60
QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMBEPPFRGRSRAPNLMQAORYGELRMSDE 120
DB 61 HCGRNGCCBPSPOLLPRDGGRRDGGAGQPFGRGRSRAPNLMQAORYGELRMSDE 120
QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWMDRNLGSGSSAPSQ 168
DB 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWMDRNLGSGSSAPSQ 168

RESULT 6
US-10-209-967-4
Sequence 4, Application US/10209967
GENERAL INFORMATION:
APPLICANT: MUNGER, JOSHUA
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
FILE REFERENCE: ARCD:380US

CURRENT APPLICATION NUMBER: US/10/209,967
CURRENT FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: 60/308,929
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 204
TYPE: PRT
ORGANISM: Mus musculus
US-10-209-967-4

Query Match 71.7%; Score 649; DB 12; Length 204;
Best Local Similarity 75.6%; Pred. No. 1.3e-48;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHROAQLMDASHOQEOPTSSSH 60
DB 43 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHROAQLMDASHOQEOPTSSSH 97
QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMBEPPFRGRSRAPNLMQAORYGELRMSDE 120
DB 98 HCGAGAVEIRSRHSSYPAGTDEDEGMBEPPFRGRSRAPNLMQAORYGELRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWMDRNLGSGSSAPSQ 168
DB 158 FEGSF-KGLPRPKSAGTATOMROSSWTRVFQSWMDRNLGSGSSAPSQ 204

RESULT 7
US-09-922-378-3
Sequence 3, Application US/09922378
Patent No. US20020037869A1
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilmann
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
FILE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 204
TYPE: PRT
ORGANISM: Mus musculus
US-09-922-378-3

Query Match 71.4%; Score 646; DB 9; Length 204;
Best Local Similarity 75.0%; Pred. No. 2.3e-48;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHROAQLMDASHOQEOPTSSSH 60
DB 43 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHROAQLMDASHOQEOPTSSSH 97
QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMBEPPFRGRSRAPNLMQAORYGELRMSDE 120
DB 98 HCGAGAVEIRSRHSSYPAGTDEDEGMBEPPFRGRSRAPNLMQAORYGELRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWMDRNLGSGSSAPSQ 168
DB 158 FEGSF-KGLPRPKSAGTATOMROSSWTRVFQSWMDRNLGSGSSAPSQ 204

RESULT 8
US-10-066-179-3
Sequence 3, Application US/10066179
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilmann

```

; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-066-179-3

Query Match          71.4%; Score 646; DB 14; Length 204;
Best Local Similarity 75.0%; Pred. No. 2,3e-48;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

Cy 1 MFQIPEFPEFSSQEDSSAERGLGPPADGPGSGGKHHRQAPGLMDASHQOEPTSSSH 60
Db 43 MFQIPEFPEFSSQEDSSAERGLGPPADGPGSGGKHHRQAPGLMDASHQOEPTSSSH 97

Cy 61 HGGAGAVEIRSRHSYPAGTEDEDEMGEBEPSPFRGRSAPPNLMAAQRVRELRMSDE 120
Db 98 HGGAGAVETRSRHSYPAGTEDEDEMGEBELSPFRGRSAPPNLMAAQRVRELRMTDE 157

Cy 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFQSWMDRLGSGSSAPSQ 168
Db 158 FEGSF-KGLPRPKSAGTATQWRQSSAGWTRITQSWMDRLGSGGSTPSQ 204

RESULT 9
US-10-059-261-258
; Sequence 258; Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 258
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TOX peptide
; US-10-059-261-258

Query Match          14.6%; Score 132; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 7,6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 103 NLMAAQRVRELRMSDEFDVDSFKK 127
Db 1 NLMAAQRVRELRMSDEFDVDSFKK 25

RESULT 10
US-09-820-843A-112
; Sequence 112; Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
```

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; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: 063915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 112
; LENGTH: 923
; TYPE: PRT
; ORGANISM: L. major
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: AC005941_2 L5204.2
; NAME/KEY: misc feature
; OTHER INFORMATION: g1|6978417
; US-09-820-843A-112

Query Match          10.6%; Score 95.5; DB 11; Length 923;
Best Local Similarity 26.4%; Pred. No. 5,7;
Matches 33; Conservative 21; Mismatches 44; Indels 27; Gaps 7;

Cy 10 SEQEDSSAERGLGPPADGPGSGGKHHRQAPGLMDASHQOEPTSSHHGAGAVEI 69
Db 802 ABQRTNTDTR---SFSAGGPASADVEHRS-----SQPQPHS---HAGGSAI-V 845

Cy 70 RSRHSYPAGTEDEDEMGEBEPSPFRGR--SRAPPNLMAAQRVRELRMSDEFDVDSFKK 127
Db 846 SNSNGVQA---SGTGRMSAANSRGRVNGSVPR-----RNGRRRAPLAIALDLTLTA 896

Cy 128 GLPRP 132
Db 897 GPQP 901

RESULT 11
US-10-071-838-6
; Sequence 6; Application US/10071838
; Publication No. US20030044814A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jing
; APPLICANT: Powers, Scott
; APPLICANT: Xiang, Phil
; APPLICANT: Peng, Yue
; APPLICANT: Tularek Inc.
; TITLE OF INVENTION: PRC17: An Amplified Cancer Gene
; FILE REFERENCE: 018781-007610US
; CURRENT APPLICATION NUMBER: US/10/071,838
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/267,615
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human PRC17 splice variant 2 (exon 10 deleted)
; US-10-071-838-6

Query Match          10.3%; Score 93.5; DB 15; Length 515;
Best Local Similarity 25.0%; Pred. No. 4,5;
Matches 41; Conservative 17; Mismatches 57; Indels 49; Gaps 8;

Cy 9 PSEQEDSSAERGLGPPADGPGSGGKHHRQ-----PGLMDASHQOEPTSSSH 60
Db 326 PAKPEQSSASR---PVPASRGKTLCKGRQAPGPAPFPRIWASPPRARSSTPC 382

Cy 61 HGGAGAVEIRSRHSYPAGTEDEDEMGEBEPSPFRGRSAPPNLMAAQRVRELRMSDE 120
Db 383 PGGA-----VRETTYVGTG-----VPSF--ALAQGPQSGKRWLQW----- 418

Cy 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVF---QSWMDRLGR 161
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Db 419 -----NSMFR-----LPTDLVEGPFRRHYDFRQSCWVRALSQ 451

RESULT 12

US-10-094-466-62

Sequence 62, Application US/10094466

Publication No. US20030203363A1

GENERAL INFORMATION:

APPLICANT: Splytek et al.

TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM

TITLE OF INVENTION: AND METHODS OF USING

FILE REFERENCE: 21402-290D

CURRENT APPLICATION NUMBER: US/10/094,466

PRIOR FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 60/274,281

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 60/288,148

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/274,849

PRIOR FILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/275,235

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: 60/338,375

PRIOR FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 60/275,579

PRIOR FILING DATE: 2001-03-13

PRIOR APPLICATION NUMBER: 60/335,302

PRIOR FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: 60/275,601

PRIOR FILING DATE: 2001-03-13

PRIOR APPLICATION NUMBER: 60/276,000

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/277,338

PRIOR FILING DATE: 2001-03-20

Prior Application data removed - See file wrapper or PALM.

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patin 2.1

SEQ ID NO 62

LENGTH: 549

TYPE: PRT

ORGANISM: Homo sapiens

US-10-094-466-62

Query Match

Best Local Similarity 10.3%; Score 93.5; DB 12; Length 549;

Matches 41; Conservative 17; Mismatches 57; Indels 49; Gaps 8;

QY 9 PSEODSSAERGLGSPAGDGPSSGSKHROA-----PGLMDASHQEOPTSSSH 60

Db 360 PAKPEQSSASR---PVPSRSGKTLCKDRQAPPPRPPRPIWSASPPRAPSSTPC 416

QY 61 HGGAGAVIRSRHSSYPAGTEDEGMBEPPFRGRSRAPNLMQAORYGRELRRMSDE 120

Db 417 PGGA-----VREDTYPVGTG-----VSP--ALAGGPGQSGWRFLOM----- 452

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVF---QSWMDRNLGR 161

Db 453 -----NSMFR-----LPTDLVVGPFWRHYDFRQSCWVRALSQ 485

RESULT 13

US-10-071-838-2

Sequence 2, Application US/10071838

Publication No. US2003004814A1

GENERAL INFORMATION:

APPLICANT: Li, Jing

APPLICANT: Powers, Scott

APPLICANT: Xiang, Phil

APPLICANT: Peng, Yue

APPLICANT: Tularik Inc.

TITLE OF INVENTION: PRC17: An Amplified Cancer Gene

FILE REFERENCE: 018781-007610US

CURRENT APPLICATION NUMBER: US/10/071,838

CURRENT FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: US 60/267,615

PRIOR FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 549

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human PRC17

US-10-071-838-2

Query Match

Best Local Similarity 10.3%; Score 93.5; DB 15; Length 549;

Matches 41; Conservative 17; Mismatches 57; Indels 49; Gaps 8;

QY 9 PSEODSSAERGLGSPAGDGPSSGSKHROA-----PGLMDASHQEOPTSSSH 60

Db 360 PAKPEQSSASR---PVPSRSGKTLCKDRQAPPPRPPRPIWSASPPRAPSSTPC 416

QY 61 HGGAGAVIRSRHSSYPAGTEDEGMBEPPFRGRSRAPNLMQAORYGRELRRMSDE 120

Db 417 PGGA-----VREDTYPVGTG-----VSP--ALAGGPGQSGWRFLOM----- 452

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVF---QSWMDRNLGR 161

Db 453 -----NSMFR-----LPTDLVVGPFWRHYDFRQSCWVRALSQ 485

RESULT 14

US-10-071-838-18

Sequence 18, Application US/10071838

Publication No. US2003004814A1

GENERAL INFORMATION:

APPLICANT: Li, Jing

APPLICANT: Powers, Scott

APPLICANT: Xiang, Phil

APPLICANT: Peng, Yue

APPLICANT: Tularik Inc.

TITLE OF INVENTION: PRC17: An Amplified Cancer Gene

FILE REFERENCE: 018781-007610US

CURRENT APPLICATION NUMBER: US/10/071,838

CURRENT FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: US 60/267,615

PRIOR FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 18

LENGTH: 549

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human PRC17.ccd1

US-10-071-838-18

Query Match

Best Local Similarity 10.3%; Score 93.5; DB 15; Length 549;

Matches 41; Conservative 17; Mismatches 57; Indels 49; Gaps 8;

QY 9 PSEODSSAERGLGSPAGDGPSSGSKHROA-----PGLMDASHQEOPTSSSH 60

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QY 61 HGGAGAVIRSRHSSYPAGTEDEGMBEPPFRGRSRAPNLMQAORYGRELRRMSDE 120

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RESULT 15
US-10-071-838-4
; Sequence 4, Application US/10071838
; Publication No. US20030044814A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jing
; APPLICANT: Powers, Scott
; APPLICANT: Xiang, Phil
; APPLICANT: Peng, Yue
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: PRC17: An Amplified Cancer Gene
; FILE REFERENCE: 018781-007610US
; CURRENT APPLICATION NUMBER: US/10/071,838
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/267,615
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human PRC17 splice variant 1 (exon 3 expanded)
US-10-071-838-4

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Query Match	10.3%	Score 93.5	DB 15	Length 610
Best Local Similarity	25.0%	Pred 5.4		
Matches 41	Conservative 17	Mismatches 57	Indels 49	Gaps 8

[illegible]

Search completed: December 29, 2003, 23:44:32
Job time : 73 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 15:12:07 ; Search time 3712 Seconds

(without alignments)
10425.783 Million cell updates/sec

Title: US-10-066-179-1

Perfect score: 946

Sequence: 1 gggcctagggcgccggtca.....gtgtgcaaaaaaaaaa 946

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_bt: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pac: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_scs: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pac: 24: em_ph: 25: em_pl: 26: em_to: 27: em_scs: 28: em_un: 29: em_vl: 30: em_hg_hum: 31: em_hg_inv: 32: em_hg_other: 33: em_hg_mus: 34: em_hg_pln: 35: em_hg_rtd: 36: em_hg_mam: 37: em_hg_vrt: 38: em_sy: 39: em_hgo_hum: 40: em_hgo_mus: 41: em_hgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	946	100.0	946	6	AR079500 Sequence
2	946	100.0	946	6	AR274069 Sequence
3	946	100.0	946	6	AX164659 Sequence
4	946	100.0	946	6	BD062656 Human BAD
5	858	90.7	948	9	BC001901 Homo sapi
6	840.4	88.8	1105	6	ARI00664 Sequence
7	840.4	88.8	1105	6	ARI66571 Sequence
8	835.4	88.3	899	9	AF021792 Homo sapi
9	799	84.5	953	6	AX329750 Sequence
10	799	84.5	953	6	HSU66879 Human Bcl-2
11	737	77.9	944	6	163695 Sequence 1
12	507	53.6	507	6	AX057144 Sequence
13	507	53.6	507	6	AF031523 Homo sapi
14	505	53.4	507	9	BT006678 Homo sapi
15	505	53.4	507	12	BT008034 Homo sapi
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17	448	47.4	174562	2	AC005848 Homo sapi
18	448	47.4	230039	2	AC090391 Homo sapi
19	437	46.2	157974	2	AP001380 Homo sapi
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21	344	36.4	1454	10	MUSBAFR L37296 Mus musculu
22	344	36.4	1472	6	AR053293 Sequence 1
23	344	36.4	1472	6	140912 Sequence 1
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25	329.6	34.8	746	6	AF031227 Rattus no
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27	327.2	34.6	615	6	AR053294 Sequence
28	327.2	34.6	615	6	140913 Sequence 3
29	325.6	34.4	615	6	AR027721 Sequence
30	325.6	34.4	615	6	AR027722 Sequence
31	324	34.2	615	6	AR027723 Sequence
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33	312.6	33.0	418	10	AF003523 Rattus no
34	267.2	28.2	445	6	AX407708 Sequence
35	245.6	26.0	338	11	G38672 SHGC-64070
36	226.8	24.0	779	10	AF279911 Rattus no
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40	195.6	20.7	2187	9	AK023420 Homo sapi
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43	187.4	19.8	189	6	AR027725 Sequence
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45	185.8	19.6	189	6	AR027727 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR079500 946 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5965703.
ACCESSION AR079500
VERSION AR079500.1 GI:10006244
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 946)
AUTHORS Horne, W.A. and Altersdorf, T.
TITLE Human bad polypeptides, encoding nucleic acids and methods of use
JOURNAL Patent: US 5965703-A1 12-OCT-1999;
FEATURES Location/Qualifiers

source 1. 946
/organism="unknown"
BASE COUNT 186 a 294 c 309 g 157 t
ORIGIN

Query Match 100.0%; Score 946; DB 6; Length 946;
Best Local Similarity 100.0%; Pred. No. 4.3e-186;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 CTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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DB 421 TCCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
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RESULT 2
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LOCUS
DEFINITION Sequence 1 from patent US 6504022.
ACCESSION AR274069
VERSION AR274069.1 GI:29706040
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Horne,W.A. and Oltersdorf,T.
TITLE Human bad polypeptides, encoding nucleic acids and methods of use
JOURNAL Patent: US 6504022-A 1 07-JAN-2003;
FEATURES
LOCATION/Qualifiers
source 1. 946
BASE COUNT 186 a 294 c 309 g 157 t
ORIGIN

Query Match 100.0%; Score 946; DB 6; Length 946;
Best Local Similarity 100.0%; Pred. No. 4.3e-186;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 1 from Patent EP1097994.
DEFINITION AX164659
ACCESSION AX164659
VERSION AX164659.1 GI:14545564
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Oltersdorf, T.
Human bad polypeptides, encoding nucleic acids and methods of use
Patent: EP 1097994-A 1 09-MAY-2001;
Idun Pharmaceuticals, Inc. (US)
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1. 946
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BASE COUNT 186 a 294 c 309 g 157 t
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Query Match 100.0%; Score 946; DB 6; Length 946;
Best Local Similarity 100.0%; Pred. No. 4.3e-186;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Human BAD polypeptides, encoding nucleic acids and methods of use.
DEFINITION BD062656
ACCESSION BD062656
VERSION BD062656.1 GI:22608259
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 946)
Horne, W.A., and Oltersdorf, T.
Human BAD polypeptides, encoding nucleic acids and methods of use
Patent: JP 2001507211-A 1 05-JUN-2001;
IDUN PHARMACEUTICALS INC
PN JP 2001507211-A/1
PD 05-JUN-2001
PF 18-SEP-1997 JP 1998514997
PR 20-SEP-1996 US 08/717123
PI WILLIAM A HORNE, TILMAN OLTERSDORF
PC C12N15/09, A61K45/00, A61P43/00, C07K14/47, C12Q1/02, G01N33/15, PC
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PC C12N15/00
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Toplogy: Linear;

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BASE COUNT 186 a 294 c 309 g 157 t

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Best Local Similarity 100.0%; Pred. No. 4.3e-186;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 901 GTACCAATGTTAATAAGCCCGGTGTGTGCCAAAAAAGAAAAA 946

RESULT 5
BC001901
LOCUS
DEFINITION
Homo sapiens, BCL2-antagonist of cell death, clone MGC:2100
IMAGE:3537914, mRNA, complete cds.

ACCESSION
BC001901
VERSION
BC001901.1 GI:12804898
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 948)
AUTHORS
Strausberg, R.
DIRECT SUBMISSION
Submitted (29-JAN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2530,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: gcaps-remail.nih.gov
Tissue Procurement: DCTD/DTF
DNA Library Preparation: Rudin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

REMARK
Seven Jones, Jennifer Asano, Ian Bosdet, Yaron Buterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ram Guin,
Leticia Hsiao, Martin Kirzysinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stolt,
Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Zetter.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 8 Row: h Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 1683636.
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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/tissue="Lung, small cell carcinoma"
/clone_id="NIH MGC 7"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
22. .528
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RGSAPSO"

BASE COUNT 209 a 302 c 289 g 148 t

ORIGIN

Query Match 90.7%; Score 858; DB 9; Length 948;
Best Local Similarity 98.0%; Pred. No. 7.8e-168;

	Matches	900; Conserved	0; Mismatches	15; Indels	3; Gaps	3
Qy	31	GATCGGGCTTGGGGCCAGAGCATGTTCACAGATCCAGAGTTTGAGCCGAGTAGAGAGAGA	90			
Db	1	GATCGGGCTTGGGGCCAGAGCATGTTCACAGATCCAGAGTTTGAGCCGAGTAGAGAGAGA	60			
Qy	91	GACTCAGCTCTGCAGAGAGGGGGCCCTGGGGCCCAAGCCCGGAGGGGAGCGGGCCCTCAGGC	150			
Db	61	GACTCAGCTCTGCAGAGAGGGGGCCCTGGGGCCCAAGCCCGGAGGGGAGCGGGCCCTCAGGC	120			
Qy	151	TCGGCAGAGCATCATCGCCAGGCCCCAGGCTCTCTGTGGAGACCGCAGTCAACAGCAGAGAG	210			
Db	121	TCGGCAGAGCATCATCGCCAGGCCCCAGGCTCTCTGTGGAGACCGCAGTCAACAGCAGAGAG	180			
Qy	211	CAGCCACCAAGACAGACGCCATCATGAGAGCGCTGTGGAGATCCGAGATCGGCAC	270			
Db	181	CAGCCACCAAGACAGACGCCATCATGAGAGCGCTGTGGAGATCCGAGATCGGCAC	240			
Qy	271	AGCTCTTACCCCGGGGGGACGAGAGACAGACGAGAGGAGTGGGGGAGAGACCCAGCCCTTT	330			
Db	241	AGCTCTTACCCCGGGGGGACGAGAGACAGACGAGAGGAGTGGGGGAGAGACCCAGCCCTTT	300			
Qy	331	CGGGGCGCTCGCGCTCGGCGGCCCCCAACCTCTGGGAGACAGACGCTATAGCCGCGAG	390			
Db	301	CGGGGCGCTCGCGCTCGGCGGCCCCCAACCTCTGGGAGACAGACGCTATAGCCGCGAG	360			
Qy	331	CTCCGAGAGATGATGACGAGATTGTGTGACTCTCTTAAGAAAGGACCTTCTCGCCGAGAG	450			
Db	361	CTCCGAGAGATGATGACGAGATTGTGTGACTCTCTTAAGAAAGGACCTTCTCGCCGAGAG	420			
Qy	451	AGCGGGGACACGACACGACATGGGGGAAAGCTCAGCTGGAGGCGAGTCTTCAGATCC	510			
Db	421	AGCGGGGACACGACACGAGATGGGGGAAAGCTCAGCTGGAGGCGAGTCTTCAGATCC	480			
Qy	511	TGTTGGAGTCGGAATTGGGACGAGGGAAGCTCCGCCCTCCAGTGACTTTCGGTCCAC	570			
Db	481	TGTTGGAGTCGGAATTGGGACGAGGGAAGCTCCGCCCTCCAGTGACTTTCGGTCCAC	540			
Qy	571	ATCCGGAATTCACACCCGTTCCATTCGCTGGGACGACCATCTGGAATATGGGCGGAAGT	629			
Db	541	ATCCGGAATTCACACCCGTTCCATTCGCTGGGACGACCATCTGGAATATGGGCGGAAGT	600			
Qy	630	AAGTTCCTCAGGAGCTATGCAAAAAGAGATCCGGTCGTATCCCTTGGAGGAGAGGTG	689			
Db	601	ACTTCCTCAGGAGCTATGCAAAAAGAGATCCGGTCGTATCCCTTGGAGGAGAGGTG	659			
Qy	690	ACCCAGATTCCTCTCCGGTGTGTGGAAGCCACGGAAG-TTGGTCCATGGAAGTTT	748			
Db	660	ACCCAGATTCCTCTCCGGTGTGTGGAAGCCACGGAAGTTTGGTCCATGGAAGTTT	719			
Qy	749	GGGTTTTCCGCCACAGCCCGCGGAAGTGGCTCGTGGCCCCCGCCCTCAGGTTTCGGGGT	808			
Db	720	GGGTTTTCCGCCACAGCCCGCGGAAGTGGCTCGTGGCCCCCGCCCTCAGGCTCGGGCT	779			
Qy	809	TTCCGCCAGGCGCTGAGCTAAGTAGAGAGCAGGTTTAACGGTTGTGACCGGGAGCC	868			
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Qy	869	GAGCCCCCGCATGCTCTGGGGCGGTGTATCAGTACCAATGTTTAATAAAGCCCGCGTGT	928			
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Qy	929	GTGCCAAAAAAGAAAAA 946				
Db	900	GTGCCAAAAAAGAAAAA 917				

RESULT 6	LOCUS	Sequence 2	1105 bp	DNA	linear	PAT 14-FEB-2001
ARI00664	ARI00664	Sequence 2 from patent US 6080847.				
ACCESSION	ARI00664	GI:1281112				
VERSION	ARI00664.1					

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1105)
TITLE	Hillman,J.L., Yue,H., Iai,P., Shab,P. and Corley,N.C.
JOURNAL	Proteins associated with cell proliferation
FEATURES	Patent: US 6080847-A 2 27-JUN-2000; Location/Qualifiers 1..1105 /organism="unknown"
BASE COUNT	209 a 368 c 352 g 176 t
ORIGIN	

Query Match	88.8%;	Score 840.4;	DB 6;	Length 1105;
Best Local Similarity	97.9%;	Pred. No. 3.4e-164;		
Matches 883;	Conservative 0;	Mismatches 16;	Indels 3;	Gaps 3;

43	GCCGAGAGCATGTTCCAGATCCGAGAGTTTGAGCGAGTGAAGCAAGATCTCCAGCT	102
Db	205 GCCAGAGCATGTTCCAGATCCGAGAGTTTGAGCGAGTGAAGCAAGATCTCCAGCT	264
Qy	103 GCAGAGAGGAGCTTGAGGCCCCAGGCCCGCAGAGGAGCGAGCCCTTAGGCTCCGCAAGCAT	162
Db	265 GCAGAGAGGAGCTTGAGGCCCCAGGCCCGCAGAGGAGCGAGCCCTTAGGCTCCGCAAGCAT	324
Qy	163 CATGCGCAGGCTCCCAAGGCTCTCTGTGGGAGCGCCAGTCAACAGCAGAGCAGCCAAACAGC	222
Db	325 CATGCGCAGGCTCCCAAGGCTCTCTGTGTGGAGCGCCAGTCAACAGCAGAGCAGCCAAACAGC	384
Qy	223 AGCAGCATCATGAGAGCGCTGAGGAGCTGTGGAGATCCGAGATCCGACAGCTCTTACCCC	282
Db	385 AGCAGCATCATGAGAGCGCTGAGGAGCTGTGTGAGATCCGAGATCCGACAGCTCTTACCCC	444
Qy	283 GCGGGAGCGAGAGCGAAGAGGATGGGGAGAGAGCCAGCCCTTTTCGGAGCGCTCG	342
Db	445 GCGGGAGCGAGAGCGAAGAGGATGGGGAGAGAGCCAGCCCTTTTCGGAGCGCTCG	504
Qy	343 CGCTCGGCTCCCCCCTTCTGTGGGACGACAGCGCTATGCGCGCAGGCTCCGAGAGATG	402
Db	505 CGCTCGGCTCCCCCCTTCTGTGGGACGACAGGCTATGCGCGCAGGCTCCGAGAGATG	564
Qy	403 AGTGAAGAGTTGTGGAGCTCCTTTAAGAGAGGACTTCTCGGCCGAGAGAGCGGGGACA	462
Db	565 AGTGAAGAGTTGTGGAGCTCCTTTAAGAGAGGACTTCTCGGCCGAGAGAGCGGGGACA	624
Qy	463 GCACAGCAGATGCGGGCAAGCTCAGCTGAGCGAGATCTTCCAGTCTGTGTGGATTCGG	522
Db	625 GCACAGCAGATGCGGGCAAGCTCAGCTGAGCGAGATCTTCCAGTCTGTGTGGATTCGG	684
-Qy	523 AACTTGGGCGAGGGAGAGCTTCGCCCCCTCCAGTGAATCTTTCGATCAATCCGGAATC	581
Db	685 AACTTGGGCGAGGGAGAGCTTCGCCCCCTCCAGTGAATCTTTCGATCAATCCGGAATC	744
Qy	582 CACCCGTTTCCATTGACCTGTGGGAGCAGCATTTTGAATTTGAGAGGAGATTAAGTTCCCTAG	641
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Qy	642 GCGTATGCAAAAAGAGGATCGTACTGTATCTTTGGAGGAGAGGTTGACCCAGATTC	701
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Db	924 CACAGCGCGGGAAGTGTGCTCGTGGGCCCGCCCTCAGGCTTCGGGGTTTTCGCCAGAGG	983
Qy	821 CTTGCGCTAAGTAGCAGAGCAGGTTTAAACGTTGTGTCAACCGGAGACCCAGAGCCCGCGA	880
Db	984 CTTGCGCTAAGTAGCAGAGCAGGTTTAAACGTTGTGTCAACCGGAGACCCAGAGCCCGCGA	1043

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Qy 881 TGCCCTGGGGGCGCTGATCAGTACCAATGTTAATAAAGCCGGGTGTGTGCCAAAAA 940
Db 1044 TGCCCTGGGGGCGCTGCTACTACCAATGTTAATAAAGCCGGGTGTGTGCCAAAAA 1103
Qy 941 AA 942
Db 1104 AA 1105

RESULT 7
LOCUS AR166571 1105 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6281334.
ACCESSION AR166571
VERSION AR166571.1 GI:16241961
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1105)
AUTHORS Hillman,J.L., Yue,H., Lal,P., Shah,P. and Corley,N.C.
TITLE Proteins associated with apoptosis
JOURNAL Patent: US 6281334-A 2 28-AUG-2001;
FEATURES
Source
Location/Qualifiers
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/organism="unknown"
BASE COUNT 209 a 368 c 352 g 176 t
ORIGIN
Query Match 88.8%; Score 840.4; DB E; Length 1105;
Best Local Similarity 97.9%; Pred. No. 3.4e-164;
Matches 883; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

Qy 43 GCCCAGACGATGTTCCAGATCCAGATTTGAGCCGAGTGAAGCAGAGAACTCCAGCTCT 102
Db 205 GCCCAGACGATGTTCCAGATCCAGATTTGAGCCGAGTGAAGCAGAGAACTCCAGCTCT 264
Qy 103 GCAGAGAGAGGAGCTGGGAGCCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 162
Db 265 GCAGAGAGAGGAGCTGGGAGCCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 324
Qy 163 CATGCGCAGGCGCCAGGCTCTGTGGAGCGCAGTCAACAGCAGAGAGAGCAGCAGC 222
Db 325 CATGCGCAGGCGCCAGGCTCTGTGGAGCGCAGTCAACAGCAGAGAGAGCAGCAGC 384
Qy 223 AGCAGCCATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 282
Db 385 AGCAGCCATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 444
Qy 283 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 342
Db 445 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 504
Qy 343 CGCTGCGGCGCCCAACCTCTGGGAGAGCAGCGCTATGCGCGAGCTCCGAGAGATG 402
Db 505 CGCTGCGGCGCCCAACCTCTGGGAGAGCAGCGCTATGCGCGAGCTCCGAGAGATG 564
Qy 403 AGTAGCAGATTGTGTGAGCTCTTTAAGAGGAGACTTCTCGGCCCAAGAGCGCGGAGCA 462
Db 565 AGTAGCAGATTGTGTGAGCTCTTTAAGAGGAGACTTCTCGGCCCAAGAGCGCGGAGCA 624
Qy 463 GCAAGCAGATGCGGCAAGGCTCAGCTGAGCGAGATCTTCCAGTCTCGTGGAGATCG 522
Db 625 GCAAGCAGATGCGGCAAGGCTCAGCTGAGCGAGATCTTCCAGTCTCGTGGAGATCG 684
Qy 523 AACTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 581
Db 685 AACTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 744
Qy 582 CACCGCTTCCATTCCTGCTGGGAGCAGCTTTTGAATATGAGGAGGAGGAGGAGGAGGAG 641
Db 745 CACCGCTTCCATTCCTGCTGGGAGCAGCTTTTGAATATGAGGAGGAGGAGGAGGAGGAG 803
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Qy 642 GCTATGCAAAAAGAGGATCCGTGCTGATCTTTGAGAGGAGGAGGAGGAGGAGGAGGAG 701
Db 804 GCTATGCAAAAAGAGGATCCGTGCTGATCTTTGAGAGGAGGAGGAGGAGGAGGAGGAG 863
Qy 702 TTCGGGTGTGTGAAGCCAGGAGG-TTGGTCCCATCGGAAGTTTGGGTTTCCGCC 760
Db 864 TTCGGGTGTGTGAAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 923
Qy 761 CACAGCCGCGGAGAGTGCTCCGTGGCGCCGCCCTCAGGTTCCGGGAGTTTCCCGCAGCG 820
Db 924 CACAGCCGCGGAGAGTGCTCCGTGGCGCCGCCCTCAGGTTCCGGGAGTTTCCCGCAGCG 983
Qy 821 CTGCGGCTAAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 880
Db 984 CTGCGGCTAAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1043
Qy 881 TGCCCTGGGGGCGCTGATCAGTACCAATGTTAATAAAGCCGGGTGTGTGCCAAAAA 940
Db 1044 TGCCCTGGGGGCGCTGCTACTACCAATGTTAATAAAGCCGGGTGTGTGCCAAAAA 1103
Qy 941 AA 942
Db 1104 AA 1105

RESULT 8
LOCUS AF021792 899 bp mRNA linear PRI 04-OCT-1997
DEFINITION Homo sapiens Bcl-X/Bcl-2 binding protein (BAD) mRNA, partial cds.
ACCESSION AF021792
VERSION AF021792.1 GI:2465410
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 899)
AUTHORS Wang,H.G., Rapp,U.R. and Reed,J.C.
TITLE Bcl-2 targets the protein kinase Raf-1 to mitochondria
JOURNAL Cell 87 (4), 629-638 (1996)
MEDLINE 97083574
PubMed 8929532
REFERENCE
2 (bases 1 to 899)
AUTHORS Takayama,S. and Reed,J.C.
TITLE Cloning of Bcl-X binding protein
JOURNAL Unpublished
AUTHORS Takayama,S., Wang,H.-G. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1997) The Burnham Inst., 10901 N. Torrey Pines
Rd., La Jolla, CA 92037, USA
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BASE COUNT 178 a 295 c 280 g 146 t
 ORIGIN

Query Match 88.3%; Score 835.4; DB 9; Length 899;
 Best Local Similarity 97.8%; Pred. No. 3.8e-163;
 Matches 878; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

QY 52 ATGTTCCAGATCCAGAGTTTGAAGCCGATGAGCAGAGAGACTCCAGCTCTGAGAGAG 111
 DB 1 ATGTTCCAGATCCAGAGTTTGAAGCCGATGAGCAGAGAGACTCCAGCTCTGAGAGAG 60

QY 112 GGCCTGGGCCCCAGCCCGGAGGGAGCGGGCCCTCAGGCTCCGGCAGCATCATGCCAG 171
 DB 61 GGCCTGGGCCCCAGCCCGGAGGGAGCGGGCCCTCAGGCTCCGGCAGCATCATGCCAG 120

QY 172 GCGCCAGGCTCTGTGGGAGCGCATGACAGCAGAGAGAGCCAGCCAGCCAT 231
 DB 121 GCGCCAGGCTCTGTGGGAGCGCATGACAGCAGAGAGAGCCAGCCAGCCAT 180

QY 232 CATGAGGCGCTGGGCTGTGAGATCCGAGATCGCCAGAGCTCTACCCCGGGAGAG 291
 DB 181 CATGAGGCGCTGGGCTGTGAGATCCGAGATCGCCAGAGCTCTACCCCGGGAGAG 240

QY 232 GAGGACGAG 351
 DB 241 GAGGACGAG 300

QY 332 CCCCCCAGCTCTGGGAG 411
 DB 301 CCCCCCAGCTCTGGGAG 360

QY 412 TTTGTGATCTCTTTAAG 471
 DB 361 TTTGTGATCTCTTTAAG 420

QY 472 ATGCGGCAAG 531
 DB 421 ATGCGGCAAG 480

QY 532 AGGGAG 590
 DB 481 AGGGAG 540

QY 591 CCATGAGCTCTGGGAG 650
 DB 541 CCATGAGCTCTGGGAG 599

QY 651 AAAAG 710
 DB 600 AAAAG 659

QY 711 GTGTGAAG 769
 DB 660 GTGTGAAG 719

QY 770 CGGAG 829
 DB 720 CGGAG 779

QY 830 AGTAG 889
 DB 780 AGTAG 839

QY 890 GGCCTGATCAGTACCAAAATGTTAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 946
 DB 840 GGCCTGATCAGTACCAAAATGTTAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896

RESULT 9
 LOCUS AX329750 953 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 259 from Patent WO1994629.
 ACCESSION AX329750

VERSION AX329750.1 GI:18102728
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endress, G.,
 Horigan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
 gene sets
 Patent: WO 0194629-A 259 13-DEC-2001;
 Avalon Pharmaceuticals (US)

TITLE
 JOURNAL
 FEATURES
 source
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BASE COUNT 172 a 321 c 300 g 160 t
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 Best Local Similarity 97.7%; Pred. No. 1.3e-155;
 Matches 874; Conservative 0; Mismatches 15; Indels 6; Gaps 6;

QY 43 GCCCAGAGATGTTCCAGATCCAGAGTTTGAAGCCGATGAGCAGAGAGACTCCAGCTCT 102
 DB 58 GCCCAGAGATGTTCCAGATCCAGAGTTTGAAGCCGATGAGCAGAGAGACTCCAGCTCT 117

QY 103 GCAG 162
 DB 118 GCAG 177

QY 163 CATGCCAG 222
 DB 178 CATGCCAG 237

QY 223 AGCAGCATCATGAG 281
 DB 238 AGCAGCATCATGAG 297

QY 282 CGCGGAG 341
 DB 298 CGCGGAG 356

QY 342 GCGCTCGGCGCCCGCAAGCTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 401
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QY 402 GAGTGAAGAGTTGTGAG 461
 DB 417 GAGTGAAGAGTTGTGAG 476

QY 462 AGCAAGCAG 521
 DB 477 AGCAAGCAG 536

QY 522 GAATCTGGGAG 580
 DB 537 GAATCTGGGAG 596

QY 591 CCACCGGTTCCATGAG 640
 DB 597 CCACCGGTTCCATGAG 655

QY 641 GGCCTATGCAAAAAG 700
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QY 701 CTTCCGAGTGTGTGAG 759
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Query Match 77.9%; Score 737; DB 6; Length 944;
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 Matches 842; Conservative 0; Mismatches 40; Indels 11; Gaps 7;

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DB 174 CATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 231
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QY 343 CCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 402
DB 352 GCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
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DB 472 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 531
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QY 582 CACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
DB 592 CACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
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RESULT 12
 AX057144 507 bp DNA linear PART 17-JAN-2001
 LOCUS AX057144
 DEFINITION Sequence 20 from Patent WO0075184.
 ACCESSION AX057144
 VERSION AX057144.1 GI:12309965
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1
 AUTHORS Zhang, H., Tsvetkov, L. M. and Kondo, T.
 TITLE Modulation of protein levels using the scf complex
 JOURNAL Patent: WO 0075184-A 20 14-DEC-2000;
 YALE UNIVERSITY (US)
 FEATURES
 source location/Qualifiers
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 BASE COUNT 99 a 165 c 175 g 68 t

Query Match 53.6%; Score 507; DB 6; Length 507;
 Best Local Similarity 100.0%; Pred. No. 5.6e-95;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 52 ATGTTCCAGATCCAGAGTTTGAAGCCAGAGAGAGAGAGAGTCCAGCTCTGAGAGAG 111
DB 1 ATGTTCCAGATCCAGAGTTTGAAGCCAGAGAGAGAGAGAGTCCAGCTCTGAGAGAG 60
QY 112 GCGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 171
DB 61 GCGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 172 GCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 231
DB 121 GCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 232 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 291
DB 181 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 292 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 351
DB 241 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 352 CCCCCAAGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
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RESULT 13
 AF031523 507 bp mRNA linear PRI 03-DEC-1997
 LOCUS AF031523
 DEFINITION Homo sapiens bcl-xL/bcl-2 associated death promoter (BAD) mRNA,
 complete cds.
 ACCESSION AF031523
 KEYWORDS

VERSION	KEYWORDS
AF031523.1	GI:2660728
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 507)
TITLE	Ottile,S., Diaz,J.L., Horne,W., Chang,S., Fritze,L.C. and Oltersdorf,T. Weeks,S., McConnell,M., Chang,S., Fritze,L.C. and Oltersdorf,T. Dimerization properties of human Bad: identification of a BH-3 domain and analysis of its binding to mutant Bcl-2 and Bcl-xL proteins
JOURNAL	J. Biol. Chem. (1997) In press
REFERENCE	2 (bases 1 to 507)
AUTHORS	Ottile,S., Diaz,J.L., Horne,W., Chang,S., Fritze,L.C. and Oltersdorf,T. Weeks,S., McConnell,M., Chang,S., Fritze,L.C. and Oltersdorf,T. Direct Submission
JOURNAL	Submitted (27-OCT-1997) IDUN Pharmaceuticals Inc., 11085 N. Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES	Location/Qualifiers
source	1..507
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	/protein_id="AAB8124.1"
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BASE COUNT	99 a 165 c 175 g 68 t
ORIGIN	
Query Match	53.6%; Score 507; DB 9; Length 507;
Best Local Similarity	100.0%; Pred. No. 5.6e-95;
Matches	507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	52 ATGTTCCAGATCCCAAGAGTTTGAGCCGAGTGCAGAGAAAGTCCAGCTTGCAGAGAG 111
DB	1 ATGTTCCAGATCCCAAGAGTTTGAGCCGAGTGCAGAGAAAGTCCAGCTTGCAGAGAG 60
QY	112 GGCCTGGGCCCCAGGCCGCGCAGAGGGAACGGGCCCTGAGCTCCGGAGAGATGATGCCAG 171
DB	61 GGCCTGGGCCCCAGGCCGCGCAGAGGGAACGGGCCCTGAGCTCCGGAGAGATGATGCCAG 120
QY	172 GCCCAGAGCTCTTGTGGGACGCCAGTCAACAGCAGAGAGCAACCAACAGCAGCAGCAT 231
DB	121 GCCCAGAGCTCTTGTGGGACGCCAGTCAACAGCAGAGAGAGCAACCAACAGCAGCAGCAT 180
QY	232 CATGAGAGCGCTGGGAGCTGTGGAGATCCGAGATCGCAAGCTCTTACCCCGGGGAGCG 291
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DB	241 GAGAGCAGAGAGAGATGGGGGAGAGAGCCCAACCCCTTTCGGGGGCGCTCCGGCTCCGAG 300
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DB	301 CCCCCAACCTTGGGACAGCAGCAGCGCTATGGCCGCGAGACTCCGGAGAGTAGTAGCAG 360
QY	412 TTGTGGAATCTTTAAGAGGGAATCTCTCGCCGAGAGAGCGCGGCAACAGCAACGAG 471
DB	361 TTGTGGAATCTTTAAGAGGGAATCTCTCGCCGAGAGAGAGCGCGGCAACAGCAACGAG 420
QY	472 ATGCGCAAGACTCCAGCTGAGACGGAAGCTTCCAGTCTTGATGGAGATGGAATCTTGGGC 531

Db	Accession	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	421	ATGGCGCAAGCTCCGAGCTGAGCGGAGCTCTCCAGTCTGTGGAGATCGAACTTGAGC	480										
Qy	532	AGGGGAAGCTCCGCGCCCTCCCACTGA	558										
Db	481	AGGGGAAGCTCCGCGCCCTCCCACTGA	507										
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LOCUS	BT006678												
DEFINITION	Homo sapiens BCL2-antagonist of cell death mRNA, complete cds.												
ACCESSION	BT006678												
VERSION	BT006678.1												
KEYWORDS	GI:30582194												
SOURCE	PII CDNA.												
ORGANISM	Homo sapiens (human)												
REFERENCE	Homo sapiens												
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.												
TITLE	1 (bases 1 to 507)												
JOURNAL	Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y., Phean, M., and Farmer, A.												
COMMENT	Cloning of human full-length CDSs in BD Creator(TM) System Donor vector												
FEATURES	Unpublished												
source	2 (bases 1 to 507)												
FEATURES	Kainthe, N., Chen, X., Rolfe, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y., Phean, M., and Farmer, A.												
COMMENT	Direct Submission												
FEATURES	Circleted (13-May-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA												
COMMENT	This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvart Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.												
FEATURES	Location/Qualifiers												
source	1..507												
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source	/lab_host="DH5alpha T1 resistant"												
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source	/product="BCL2-antagonist of cell death"												
FEATURES	/protein_id="AAP5324.1"												
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FEATURES	/translation="MPOIPPEPESEORSSAERGLGSPAGDPSGSKHNRAPGILMDSSHOOEPTSSHHGAGAVHTRKSHSYPRGTDDDEMGEBEPFRFRSSAPPLNMAQRYGRRLRMDSDFVDSFKGJLPRPSAGTATVOMROSSSWTVFPOMDRNLDRGSSAPSO"												
BASE COUNT	99 a 165 c 175 g 68 t												
QUALITY	Query Match 53.4%; Score 505; DB 9; Length 507; Best Local Similarity 100.0%; Pred. No. 1.5e-94; Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					</							

QY 112 GGCCTGGGCCCCAGCCCCGAGGGAGCGGGCCCTCAGGCTCCGGCAGCATCATGCCAG 171
DB 61 GGGCTTGGGGCCCCAGCCCCGAGGGAGCGGGCCCTCAGGCTCCGGCAGCATCATGCCAG 120
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QY 232 CATGAGAGGCGCTGGGAGTGGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAG 291
DB 181 CATGAGAGGCGCTGGGAGTGGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAG 240
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DB 241 GAGGACGAGGAGGAGTGGGAGGAGAGCCAGCCCTTTTCGAGGCGCTCGCGCTGGGCG 300
QY 352 CCCCCCAACTCTGGGAGCAGCAGCGCTATGCGCGGAGCTCCGAGAGATGATGACGAG 411
DB 301 CCCCCCAACTCTGGGAGCAGCAGCGCTATGCGCGGAGCTCCGAGAGATGATGACGAG 360
QY 412 TTTGTGACTCTTTAAGAGGAGTCTTCTCGCCGAGAGGCGGGGAGCAGCAGCAGCAG 471
DB 361 TTTGTGACTCTTTAAGAGGAGTCTTCTCGCCGAGAGGCGGGGAGCAGCAGCAGCAG 420
QY 472 ATGCGGCAAGCTCCAGCTGAGCGCGAGTCTTCTCAGTCTGAGTGGAGTGGAACTTGGGC 531
DB 421 ATGCGGCAAGCTCCAGCTGAGCGCGAGTCTTCTCAGTCTGAGTGGAGTGGAACTTGGGC 480
QY 532 AGGGGAAGCTCCGCGCCCTCCCACT 556
DB 481 AGGGGAAGCTCCGCGCCCTCCCACT 505

RESULT 15

LOCUS BT008034 507 bp mRNA linear SYN 13-MAY-2003
DEFINITION Synthetic construct Homo sapiens BCL2-antagonist of cell death
ACCESSION BT008034
VERSION BT008034.1 GI:30584906
KEYWORDS FLI CDNA.
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 507)
AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,
Pheasant,M. and Farmer,A.
TITLE Cloning of human full-length CDS in BD Creator(TM) System Donor
vector
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 507)
AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,
Pheasant,M. and Farmer,A.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 Bascom
COMMENT Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: <http://bioinfo.clontech.com/orfclones>.
Location/Qualifiers
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/db_xref="taxon:32630"

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BASE COUNT 98 a 165 c 175 g 69 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1,56-94;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 ATGTTCCAGATCCAGAGTTTGAAGCCGAGTGAAGAGAGAACTCCAGCTTGCAGAGAG 111
DB 1 ATGTTCCAGATCCAGAGTTTGAAGCCGAGTGAAGAGAGAACTCCAGCTTGCAGAGAG 60
QY 112 GGCCTGGGCCCCAGCCCCGAGGGAGCGGGCCCTTAAGGCTCCGAGATCATGATGCCAG 171
DB 61 GGCCTGGGCCCCAGCCCCGAGGGAGCGGGCCCTTAAGGCTCCGAGATCATGATGCCAG 120
QY 172 GCGCCAGGCTCTCTGGGAGCGGAGTCAACAGCAGAGCAGCAGCAGCAGCAGCAGT 231
DB 121 GCGCCAGGCTCTCTGGGAGCGGAGTCAACAGCAGAGCAGCAGCAGCAGCAGCAGT 180
QY 232 CATGAGAGGCGCTGGGAGTGGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAG 291
DB 181 CATGAGAGGCGCTGGGAGTGGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAG 240
QY 292 GAGGACGAGGAGGAGTGGGAGGAGAGCCAGCCCTTTTCGAGGCGCTCGCGCTGGGCG 351
DB 241 GAGGACGAGGAGGAGTGGGAGGAGAGCCAGCCCTTTTCGAGGCGCTCGCGCTGGGCG 300
QY 352 CCCCCCAACTCTGGGAGCAGCAGCGCTATGCGCGGAGCTCCGAGAGATGATGACGAG 411
DB 301 CCCCCCAACTCTGGGAGCAGCAGCGCTATGCGCGGAGCTCCGAGAGATGATGACGAG 360
QY 412 TTTGTGACTCTTTAAGAGGAGTCTTCTCGCCGAGAGGCGGGGAGCAGCAGCAGCAG 471
DB 361 TTTGTGACTCTTTAAGAGGAGTCTTCTCGCCGAGAGGCGGGGAGCAGCAGCAGCAG 420
QY 472 ATGCGGCAAGCTCCAGCTGAGCGCGAGTCTTCTCAGTCTGAGTGGAGTGGAACTTGGGC 531
DB 421 ATGCGGCAAGCTCCAGCTGAGCGCGAGTCTTCTCAGTCTGAGTGGAGTGGAACTTGGGC 480
QY 532 AGGGGAAGCTCCGCGCCCTCCCACT 556
DB 481 AGGGGAAGCTCCGCGCCCTCCCACT 505

Search completed: December 29, 2003, 16:20:19
Job time : 3721 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 22:31:04 / Search time 85 Seconds
(without alignments)
510.033 Million cell updates/sec

Title: US-10-066-179-2

Perfect score: 905
Sequence: 1 MFOIPEFPPSEQEDSSSAER.....RVFGSWMDNLGRGSSAPSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTREMBL_23.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rickettsia.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_virus.*
- 17: sp_bacteriophage.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	100	11.0	608	12	Q9Q5K9 herpessvirus
3	98.5	10.9	569	13	Q9DF20 Q9DF20
4	98.5	10.9	669	11	Q8CC96 mus musculus
5	98	10.8	272	4	Q9NS37 Q9NS37
6	98	10.8	355	16	Q9RDL8 Q9RDL8
7	98	10.8	501	4	Q9ED83 Q9ED83
8	97.5	10.8	867	10	Q9FV26 Q9FV26
9	97	10.7	1146	5	Q9N8Q9 Q9N8Q9
10	96.5	10.7	980	4	Q9S387 Q9S387
11	96.5	10.7	2506	4	Q9NS88 Q9NS88
12	95.5	10.6	349	6	Q8HY95 Q8HY95
13	95.5	10.6	923	5	Q8KX14 Q8KX14
14	95.5	10.6	923	5	Q9NKN4 Q9NKN4
15	95	10.5	622	4	Q9NTR2 Q9NTR2
16	95	10.5	701	4	Q9NTP8 Q9NTP8

17	95	10.5	803	4	Q9ULK9 Q9ULK9
18	94.5	10.4	650	11	Q8BWB8 Q8BWB8
19	94	10.4	494	5	Q9VA96 Q9VA96
20	94	10.4	581	10	Q8S7B1 Q8S7B1
21	93.5	10.3	549	4	Q9H0B9 Q9H0B9
22	93.5	10.3	549	4	Q8I2P1 Q8I2P1
23	93.5	10.3	1727	4	Q9UPQ9 Q9UPQ9
24	93.5	10.3	1729	4	Q25734 Q25734
25	93	10.3	682	11	Q8BME5 Q8BME5
26	93	10.3	1300	12	Q36421 Q36421
27	93	10.3	2472	4	Q9NS89 Q9NS89
28	92.5	10.2	336	12	Q98321 Q98321
29	92	10.2	1454	12	Q8JL63 Q8JL63
30	91.5	10.1	415	12	Q91TH4 Q91TH4
31	91.5	10.1	651	4	Q9NX19 Q9NX19
32	91.5	10.1	845	4	Q9HAU3 Q9HAU3
33	91.5	10.1	990	4	Q15206 Q15206
34	91.5	10.1	1218	4	Q05331 Q05331
35	91	10.1	349	6	Q8HY96 Q8HY96
36	91	10.1	494	5	Q8T8V0 Q8T8V0
37	90.5	10.0	309	5	Q8UK99 Q8UK99
38	90.5	10.0	704	5	Q9VW76 Q9VW76
39	90.5	10.0	708	4	Q96JH4 Q96JH4
40	90.5	10.0	947	10	Q9LWJ9 Q9LWJ9
41	90.5	10.0	1319	5	Q95X47 Q95X47
42	90	9.9	476	10	Q8W0Z0 Q8W0Z0
43	90	9.9	476	10	Q9FFH8 Q9FFH8
44	90	9.9	903	4	Q9UPX1 Q9UPX1
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ALIGNMENTS

RESULT 1	Q919N2	PRELIMINARY;	PRT;	146 AA.
AC	Q919N2			
DT	01-OCT-2000 (TRENBLREL. 15, Created)			
DT	01-DEC-2001 (TRENBLREL. 19, Last sequence update)			
DT	01-OCT-2002 (TRENBLREL. 22, Last annotation update)			
DE	Bad.			
GN	Brachydanio rerio (zebrafish) (Danio rerio).			
OS	Brachydanio rerio (zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20373792; PubMed=10917738;			
RA	Inohara N., Nunez G.;			
RT	"Genes with homology to mammalian apoptosis regulators identified in			
RT	zebrafish."			
RL	Cell Death Differ. 7:509-510(2000).			
DR	EMBL: AF231017; AAF66962.2; -			
DR	HSSP; Q92934; 165J.			
ZFIN	ZDB-GENE-000616-1; bad.			
SQ	SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;			
Query Match	23.8%; Score 215.5; DB 13; Length 146;			
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QY	1 MFOIPEFPPSE-----QEDSSAERGLGSPAGDPSGSGKHRAQGLLWDASHQOEPT 56			
DB	4 MFNISDSDETFETWSESDSLDKKSG-----SAQKXGHLTVPRDL-----KGEQ-- 48			
QY	57 SSSHHGAGAVIRSRHSYAGTED--DEMGSEPP-----SPFGKSSASAPNLMAGRY 110			
DB	49 -----LGRQNLKSWNEBLLLETGVADPHMLGDPFRSRSSAPPALMAAKY 95			
QY	111 GRELRMSDEFVDSFKKGLPRPKSAGTATQKRGSSSWTRVQSWMDNLGRGSSAPSQ 168			

Db 96 GQARRMSDE----FDKMKRKKVKSAGTARQKSGSPSWIAFL---WSHKESDAESRPAP 146

RESULT 2

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AC Q9QSK9
DT 01-MAR-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE NTR.
OS Herpesvirus papio.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.

NCBI_TaxID=10394;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=Baboon lymphocryptovirus BA65;
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,
RA Hayward G.S.;

RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF200364; AAF23950.1; --
SQ SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;

Query Match 11.0%; Score 100; DB 12; Length 608;

Best Local Similarity 33.3%; Pred. No. 0.67;

Matches 37; Conservative 7; Mismatches 55; Indels 12; Gaps 3;

Qy 9 PSEGEDSSAERGLGSPAGDPSGSGKHROAPGLMDASHOQPTSSHHG---GA 64

Db 502 PRTRRRRSAGRGHPGAGGPGSGTGHAPAPGAPGPRPRTRRRRSAGRGHPG 561

Qy 65 GAVETRSHSSYPAGTEDEGMEGPEPSPRRGRSRAPNMAQRXGREL 115

Db 562 G-----QPPSGPTGHPAPAPGPPNPERGSGPADP---AATLPLEPR 604

RESULT 3

Q9DF20 PRELIMINARY; PRT; 569 AA.

AC Q9DF20
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)

DE KH domain containing RNA-binding protein FMRL.

GN FMRL.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.
RC MEDLINE=20501263; PubMed=11046149;
RA Wan L., Dockendorff T.C., Jongs T.A., Dreyfuss G.;

RT "Characterization of dFMR1, a Drosophila melanogaster Homolog of the
RT Fragile X Mental Retardation Protein.;"

RL Mol. Cell. Biol. 20:8536-8547(2000).

CC -1- SIMILARITY: CONTAINS 2 KH DOMAINS.

DR EMBL; AF305882; AAC22046.1; --
DR HSSP; Q06787; 2FMR.

DR ZFIN; ZDB-GENE-020731-6; fmrl.
DR InterPro; IPR004087; KH_dom.

DR InterPro; IPR004088; KH_type_1.
DR Pfam; PF00013; KH; 2.

DR SMART; SM00322; KH; 2.
DR PROSITE; PS50084; KH TYPE 1; 2.

SQ SEQUENCE 569 AA; 63906 MW; 2B6A06897EDFB5 CRC64;

Query Match 10.9%; Score 98.5; DB 13; Length 569;

Best Local Similarity 32.3%; Pred. No. 0.85;

Matches 31; Conservative 8; Mismatches 42; Indels 15; Gaps 3;

Qy 11 EODSSAERGLGSPAGDPSGSGKHROAP-----GLMDASHOQPTSSHHGAGA 66

Db 391 EKEKSPWADNGWSPRGCKPFRGCGRGRCPLTASGTSEANASG--TESDH----- 442

Qy 67 VEIRSRHSYPAGTEDEGMEGPEPSPRRGRSAPP 102

Db 443 ---RDELSDWSLAPTDEESWGYPRAPDGRKRGCGP 475

RESULT 4

Q8CC96 PRELIMINARY; PRT; 669 AA.

AC Q8CC96
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RA MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.;"

RL Nature 420:563-573(2002).

DR EMBL; AK035885; BAC28374.1; --
KW Hypothetical protein.

SQ SEQUENCE 669 AA; 72969 MW; 1E30636A45FEB39B CRC64;

Query Match 10.9%; Score 98.5; DB 11; Length 669;

Best Local Similarity 25.8%; Pred. No. 1;

Matches 51; Conservative 25; Mismatches 63; Indels 59; Gaps 10;

Qy 1 MFOIFEPPEBOE-DSSAER-GLGSPAGDPSGSGKHROAPGLMDASHOQPTSS 58

Db 412 LLOASBERGEOEQAOEAERAGENPTPAKGVKSQVKSMLRASFIRKHSKSKKTEA 471

Qy 59 SHHGAGAVEIR-----SRH-----SSYPAGTE--DDEGMEEP-----SPFG 95

Db 472 SCTPGSSLEAPPRKKGFLPMCVSGHRASISSPESELEQKTEAAGAGAGSGAPFGA 531

Qy 96 RSRS-----APPNMAAQRX-----GREIR-----RMSDEFYDSFKKG 128

Db 532 RSHTPDEGSPERAMBSKEFWIQTLVASLQEVDRDLGRQIRKYPSPFRFNEFSDASLRK 591

Qy 129 LPRKASGTATQMGROSS 146

Db 592 L-----VATLEROKAS 602

RESULT 5

Q9NS37 PRELIMINARY; PRT; 272 AA.

AC Q9NS37
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)

DE HCF-binding transcription factor Zhangfei.
GN ZF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20330366; PubMed=10871379;
RX Lu R., Miera V.;

RT "Zhangfei: a second cellular protein interacts with herpes simplex
virus accessory factor HCF in a manner similar to human and VP16."
RL Nucleic Acids Res. 28:2446-2454(2000).
CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.
DR EMBL: AF039942; AAD28325.1; -.
DR InterPro: IPR004827; TF_BZIP.
DR Pfam: PF00170; bZIP; 1.
DR SMART: SM00338; BRLZ; 1.
DR DNA-binding; Nuclear protein.
SQ SEQUENCE 272 AA; 28859 MW; B1F94B438F0702BF CRC64;

Query Match 10.8%; Score 98; DB 4; Length 272;
Best Local Similarity 28.2%; Pred. No. 0.4;
Matches 40; Conservative 13; Mismatches 69; Indels 20; Gaps 4;

QY 10 SEGEDSSAERGLGSPGAGGSGGKHROAPGLMDASHQOEOPITSSHHGAGAVEI 69
DB 92 SSSSDSGSAKRRKSPGGGGGGGNDNNQA-----ATKSPRKAAANAARL 138
QY 70 -RSRHSSYPAGTEDD-EGMGEEPSPPGRGRSAPPNMAQRYGRELRRMSDEFVDSFK 127
DB 139 NNLKKEEYWGLESRRGLAENQELRAENRLEKRYVALQESRYLRA-----VLANET 193
QY 128 GLPRPSAGTATQMRQSSSWTR 149
DB 194 GLARLRLSGVGLRLTTLR 215

RESULT 6

Q9RDL8 PRELIMINARY; PRT; 355 AA.

AC Q9RDL8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative DNA-binding protein.
GN SC02568 OR SCC123.06C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.
OX NCBI_Taxid=1902;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleier H.M., Denapate D., Eichner A., Cullum J.,
RA Kinoshita H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome";
RL Mol. Microbiol. 21:77-96(1996).
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleier H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieiser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabnowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)";
RL Nature 417:141-147(2002).
DR EMBL: AL939113; CAB6246.1; -.
DR InterPro: IPR000445; HhH.
DR InterPro: IPR003583; HhH_1.
DR Pfam: PF00633; HhH; 1.
DR SMART: SM00278; HhH1; 1.
DR DNA-binding; Complete proteome.
SQ SEQUENCE 355 AA; 36853 MW; E1E9DA574CCABDE CRC64;

Query Match 10.8%; Score 98; DB 16; Length 355;
Best Local Similarity 28.5%; Pred. No. 0.54;
Matches 43; Conservative 14; Mismatches 66; Indels 28; Gaps 7;

QY 15 SSAERGLGSPGAGGSGGKHROAPGLMDASHQOEOPITSSHHG--GAGAVEIRSR 72
DB 9 TASATSGPRADAPASDRLA---HRRAPGSRTHAHR-----SHARHGRHAAPELRRR 59
QY 73 -HSSYPAGTEDDEGMEGEEPSPPGRGRSAP--PNLMAQRYGRELRRMSDEFVDSFKGL 129
DB 60 AETLFAERAGYDHAHGEGA--HGETGKGPPLGLDAPARQGSPL-----PGL 105
QY 130 PRPSAGTATQMRQSSSWTRVFQSWDRNIG 160
DB 106 DAPRGRTMRERAGSALRRMPWLQTRCG 136

RESULT 7

Q96D83 PRELIMINARY; PRT; 501 AA.

AC Q96D83;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Straussberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010283; AAH10283.1; -.
KW Hypothetical protein.
SQ SEQUENCE 501 AA; 53710 MW; E0813BC41923F2DE CRC64;

Query Match 10.8%; Score 98; DB 4; Length 501;
Best Local Similarity 24.4%; Pred. No. 0.81;
Matches 43; Conservative 16; Mismatches 83; Indels 34; Gaps 7;

QY 3 QIPEPESEEDSSAERGLGSP-----SPAGDGP--SGSGKHROAPGLMDASHQOE 53
DB 334 EPRREGRKPSDWDGNRPBGHGFHFDTPRPDPHIDGHPARERSSSLQGMDSL 393
QY 54 OPTSSHHGAGAVEIRSRHSSYPAGTEDDEGMEGEEPSPPGRGRSAPPNLMAQRYGRE 113
DB 394 PPRKRPMHDGPTSHREWEA--FCGPSEDRG-----CKGRGCPQAPQRPVKSGRS 442
QY 114 LRMSDEFVDSFKGLP--RKSAGTATQMRQSSSWTRVFQSWDRNIGRGSSAS 167
DB 443 -SSLDEHHDGYHRDEPGPGPGSGTSPRGRSGS-----NMGGRGNNMS 486

RESULT 8

Q9FVZ6 PRELIMINARY; PRT; 867 AA.

AC Q9FVZ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

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DE Putative replication protein.
GN OSUNB0073N24.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buehl C.R., Yuan Q., Mofatt K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA HeLaio J., Ziemann V., Pal G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalaf H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSUNB0073N24 genomic sequence.";
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC078840; AAG13631.1; -.
DR Gramene; Q9FVZ6; -.
SQ SEQUENCE 867 AA; 94083 MW; 4FEA69E1BFCC0B2C CRC64;

Query Match 10.8%; Score 97.5; DB 10; Length 867;
Best Local Similarity 28.0%; Pred. No. 1.7;
Matches 37; Conservative 10; Mismatches 46; Indels 39; Gaps 5;

QY 13 EDSSSAERGLGPPSPAG---DGPSSGSGKHHROAP-----GILMDASHQOE--- 53
DB 730 KEBAARAGGGPDDLPLSHSLGCGGTGKEAAAPPTRGASRGCGGADADAGSEQEDAA 789
QY 54 -----QPTSSHHGAGAVEIRSHSSYPAGTEDEGMEPEPFPFRGRSAPPNLMMA 107
DB 790 AMGGPPPLSHSLGCGG-----GTGKEA-AAAPPTRGASRGCGGCGGTGT 835
QY 108 ORYGELELRMSD 119
DB 836 REERRLGRKEE 847

RESULT 9
Q9N8Q9 PRELIMINARY; PRT; 1146 AA.
ID Q9N8Q9
AC Q9N8Q9
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Possible calpain-like protease.
GN CH11.189.
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Leonard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerard C., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL929605; CAB95474.1; -.
DR InterPro; IPR001300; Protease_C2.
DR Pfam; PF00648; Peptidase_C2; 1.
DR SMART; SM00230; Cyspc; 1.
DR KEGG;
SQ SEQUENCE 1146 AA; 126154 MW; 89FC26E43768B3F CRC64;

Query Match 10.7%; Score 97; DB 5; Length 1146;
Best Local Similarity 23.2%; Pred. No. 2.7;
Matches 46; Conservative 18; Mismatches 90; Indels 44; Gaps 7;

QY 6 EFBPEQDSSAERGLGPPSPAG---DGPSSGSGKHHROAPGILMDAS 49
DB 80 ESEAVEGSDGRRAEASPAAPSGESDEKASKEHSEYKESDGAERASPAAPS---PAG 136
QY 50 HQEOPTSSSH---HGAGAVEIRSHSSYPAGTEDD-----EGMGEE 89

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DB 137 ESDKASKSESEYKESDGRRAEASPAAPS-PAGESDEKASKEHSEYKESDGRRAE 195
QY 90 PSPFRGSRGAPPNLMMAORYGRELRMSDEYFDSFKGLPRPKSAGTATOMQSSWTR 149
DB 196 ASRAPSPAGSDDEKA-SKSEHSEYKESD---DRAEASPAAPSGESDEKASKSEHSE 251
QY 150 VFQSWMDRNLGRSSAPS 167
DB 252 EAKESDGRRAEASPAAPS 269

RESULT 10
Q95387 PRELIMINARY; PRT; 980 AA.
ID Q95387
AC Q95387
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Voltage-dependent P/Q type calcium channel alpha 1A subunit
DE (Fragment).
GN CACNA1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Black J.L., Snutch T.P., Lennon V.A.;
RT "Partial sequence of Homo sapiens P/Q-type voltage-gated calcium
RT channel alpha 1 (alpha 1A) subunit isolated from small cell lung
RT carcinoma cell line, SCC 9, cDNA library.";
RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF100774; AAC7460.1; -.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Ca_channel_TrypL.
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M_channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR00167; CACHANNEL.
KM Ionic channel; Transmembrane.
FT NON_TER
SQ SEQUENCE 980 AA; 110251 MW; AF627D9F8BE16D43 CRC64;

Query Match 10.7%; Score 96.5; DB 4; Length 980;
Best Local Similarity 25.1%; Pred. No. 2.5;
Matches 46; Conservative 16; Mismatches 50; Indels 69; Gaps 10;

QY 15 SSSAERGLGPPSP---AGDGPSSGSGKHHROAP-----GILMDAS- 49
DB 809 TSGPRRYPTAEDPLADGDRPTTGSHSGSRSPRMERVRVGPASRSPRACHRGARWPASG 868
QY 50 -HQEOPTSSSHHGAGAVEIRSHSSYPAGTEDE-----GMGE-----PSPFR 94
DB 869 PHYSEGGPPGPRHHG-----YRGSVDDEADGPGSGGGEAMAGAYDAPPVR 915
QY 95 -----GRS-----RSAPPNLMMAORYGRELRMSDEYFDSFKGLPRPKSAGTATOMQ 143
DB 916 HASSGATGRSPRTTRAGSPACASPRIG---RLPNQYRA--HGLARPPGSGSKGLHE 970
QY 144 SSS 146
DB 971 PYS 973

RESULT 11
Q9NS88 PRELIMINARY; PRT; 2506 AA.
ID Q9NS88
AC Q9NS88
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha1-voltage-dependent calcium channel.

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GN CACNA1A.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TTSUB=Cerebellum;
RA MEDLINE=20219126; PubMed=10753886;
RA Toru S., Murakoshi T., Ishikawa K., Saegusa H., Fujigasaki H.,
"Uchiyama T., Nagayama S., Osana M., Mizusawa H., Tanabe T.,
"Sphincterbellar ataxia type 6 mutation alters P-type calcium channel
function.";
RT J. Biol. Chem. 275:10893-10898 (2000).
RL EMBL; AB035727; BAA94766.2; -
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Ca_channel_TrypL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005448; PVDCCALphal.
DR Pfam; PF00520; ion_trans; 4.
DR PRINTS; PR00167; CACNANL.
DR PRINTS; PR01632; PVDCCALPHAL.
DR SMART; SM00384; AT hook; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 2506 AA; 282579 MW; D64AC75284A1B53 CRC64;

Query Match 10.7%; Score 96.5; DB 4; Length 2506;
Best Local Similarity 25.1%; Pred. No. 7.4;
Matches 46; Conservative 18; Mismatches 50; Indels 69; Gaps 10;

15 SSSAERGIGPSP---AGDGPSSGSKHROAP-----GLMDAS- 49
Db 2335 TGGPRYPGPPTAPPLGDRPPGCHSSGSPMERVPBPAPASESPRACHGAPWPSG 2394
Qy 50 -HQEQPTSSHHGAGAVEIRSRHSSYPAGTEDE-----QMGEE-----PSPPR 94
Db 2395 PHVSEGPSPRRHG-----YRGSYDLDADPGSGGHEAMAGAYDAPPPV 2441
Qy 95 -----GRS-----RSAPNLMQAQRYGELRRMSDFVDSFKKGLPRPSAGTATQMQ 143
Db 2442 HASSGATGRSPTRPRASGPACASPSRHG---RRLPGYVPA--HGLAPRPGSRKGLHE 2496
Qy 144 SSS 146
Db 2497 PYS 2499

RESULT 12
Q8HY95 PRELIMINARY; PRT; 349 AA.
ID Q8HY95;
AC Q8HY95;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Dentin matrix protein 1 (Fragment).
GN DMP1.
OS Thysanoptera tricolor (Spix's disk-winged bat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Thyropteridae;
OC Thysanoptera.
OX NCBI_TaxID=124759;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22359429; PubMed=12470941;
RA Van Den Bussche R.A., Reeder S.A., Hansen E.W., Hoofe S.R.;
"Utility of the dentin matrix protein 1 (DMP1) gene for resolving
mammalian intraordinal phylogenetic relationships.";
RT Mol. Phylogenet. Evol. 26:89-101 (2003).
RL EMBL; AV141890; AAN75483.1; -
KW Matrix protein.

FT NON TER 1 1
FT NON TER 349 349
SQ SEQUENCE 349 AA; 37953 MW; 0B12698CB2E25C77 CRC64;
Query Match 10.6%; Score 95.5; DB 6; Length 349;
Best Local Similarity 24.7%; Pred. No. 0.9;
Matches 38; Conservative 21; Mismatches 48; Indels 47; Gaps 7;
Qy 3 QPPEPSPSE-----QEDSSAERGLGSPAGDGPSSGSKHROAPGLMDASHOE----- 53
Db 217 QPPEPSPSEVLPQOFTSSSQOBLVSTPRGDNDPNTSSHEVPE---DSDSFEEDLU 273
Qy 54 -QPTSSHHGAGAVEIRSRHSSYPAGTEDEDEGMBEPSPFRGRSAPNLMQAQRYGR 112
Db 274 NEPSSS-----ESNREREO--ADSESNLSL-----KYSB 300
Qy 113 ELRRMSDFVDSFKKGLPRPSAGTATQMQRSS 146
Db 301 ESPESTEBENSSQOGLQSP-SASASRSSESSQS 333

RESULT 13
Q8MXL1 PRELIMINARY; PRT; 923 AA.
ID Q8MXL1;
AC Q8MXL1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE L5204.2.
GN L5204.2.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Frledlin;
RA Worthey E.A., Sisk E., Hixson G., Kiser P., Richel E., Haesebrock M.,
Cawthra J., Sunkin S., Stuart K.D., Myler P.J.;
"Direct Submission";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC125735; AAM68998.1; -
DR InterPro; IPR000533; TROPOMYOSIN.
DR PRINTS; PR00194; TROPOMYOSIN.
SQ SEQUENCE 923 AA; 104025 MW; C232C0E464B0F6C7 CRC64;

Query Match 10.6%; Score 95.5; DB 5; Length 923;
Best Local Similarity 26.4%; Pred. No. 2.8;
Matches 33; Conservative 21; Mismatches 44; Indels 27; Gaps 7;

Qy 10 SFOEDSSAERGLGSPAGDGPSSGSKHROAPGLMDASHOQOQPTSSHHGAGAVEI 69
Db 802 AEQRTNTDDR---SPSAGPASPADVHERSA-----SQPQPHS---HAGSAI-V 845
Qy 70 RSRHSSYPAGTEDEDEGMBEPSPFRGR--SRAPNLMQAQRYGELRRMSDFVDSFKK 127
Db 846 SNSHNGVQAAA---SCTGRMGAANGRGVNGSVPP-----RNGRRRAPLAALIDITLTA 896
Qy 128 GLPRP 132
Db 897 GPPQP 901

RESULT 14
Q9NKN4 PRELIMINARY; PRT; 923 AA.
ID Q9NKN4;
AC Q9NKN4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE L5204.2.
GN L5204.2.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hasebrock M.,
CAWthra J., Marsolini F., Sunkin S., Stuart K.D.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005941; AAF34290.1; -
DR InterPro; IPR000533; Tropomyosin.
DR PRINTS; PRO0194; TROPOMYOSIN.
SQ SEQUENCE 923 AA; 103964 MW; C229C15F6448F7C7 CRC64;

Query Match 10.6%; Score 95.5; DB 5; Length 923;
Best Local Similarity 26.4%; Pred. No. 2.8;
Matches 33; Conservative 21; Mismatches 44; Indels 27; Gaps 7;

QY 10 SEQDSSAERGLGSPAGDDPGSGSKHROAPGLMDASHQEOPTSSHHGAGAVEI 69
DB 802 AEQRTNTDDR-----SPSAGGPASADVEHRS-----SQPOQPHS---HAGSAL-V 845
QY 70 RSRSSYPAGTEDEDEGMEEPSPPFGR--SRSAPPNLMAQRYGRELRLMSDEFVDSFKK 127
DB 846 SNSHNGVQAAA---SGTGRMSAANSGRVNGSVPP-----RNGRRRAPLAALIDITLTA 896
QY 128 GLPRP 132
DB 897 GPQP 901

RESULT 15

Q9NTE2 PRELIMINARY; PRT; 622 AA.
ID Q9NTE2;
AC Q9NTE2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP434B239.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Pousetta A., Klein M., Mewes H.W., Gaassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137336; CAB70699.1; -
KW Hypothetical protein.
FT NON TER.
SQ SEQUENCE 622 AA; 67337 MW; 11D6CDF0E2D06082 CRC64;

Query Match 10.5%; Score 95; DB 4; Length 622;
Best Local Similarity 27.6%; Pred. No. 2;
Matches 50; Conservative 17; Mismatches 50; Indels 64; Gaps 11;

QY 13 EDSSAERGLGSP--AGDPSGSGKHROAPGLMDASHQEOPTSSHHGAGAVEI 69
DB 14 EKKHAEPAPAGBNPPRGDARAGSK-----AKPPQESPSSAS--ALAEWASI 60
QY 70 RSR-----HSSYPAGTEDEDE-GMEEPSP-----FRGRSRAP-----NLMAQRY--- 110
DB 61 RSRILKNAESDPRSERQDLRPGDESTRGRCDSKGNCRKTPPVNAKFSIMPWQKFSDG 120
QY 111 GRELRMSDEFVDSFKK-----GLPRKSAGTATQMROSSWTVFQSWMDRLNGR 161
DB 121 GTEYSKOSTE-AESIRKRPMLGPSETAPQPPAGV-----RELGX 160
QY 162 G 162
DB 161 G 161

Search completed: December 29, 2003, 23:34:42
Job time : 92 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 17:04:24 ; Search time 75 Seconds
(without alignments)
355.548 Million cell updates/sec

Title: US-10-066-179-2

Perfect score: 905
Sequence: 1 MFQIPEFEPSEQEDSSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	905	100.0	168	19	AAW55779
2	905	100.0	168	21	AAW55779
3	905	100.0	168	22	AAW55779
4	905	100.0	168	22	AAW55779
5	905	100.0	168	22	AAW55779
6	905	100.0	168	22	AAW55779
7	864	95.5	201	23	ABP41630
8	751	83.0	166	18	AAW32476
9	649	71.7	162	22	AAW70370

10	649	71.7	204	17	AAW95168	bcl-x(l)/bcl-2 ass
11	649	71.7	204	19	AAW61315	Mutant BCL-XL/BCL-
12	649	71.7	204	19	AAW58832	Murine BAD protein
13	649	71.7	204	22	AAW70369	Longer murine BAD
14	649	71.7	204	24	ABR39082	Murine BAD protein
15	646	71.4	204	19	AAW61317	Mutant BCL-XL/BCL-
16	643	71.0	204	19	AAW61316	Mutant BCL-XL/BCL-
17	643	71.0	204	19	AAW61318	Mutant BCL-XL/BCL-
18	643	71.0	567	22	AAU00220	Bad-DTRR apoptosis
19	314	34.7	59	19	AAW61319	Mutant BCL-XL/BCL-
20	314	34.7	59	19	AAW61320	Mutant BCL-XL/BCL-
21	311	34.4	59	19	AAW61321	Mutant BCL-XL/BCL-
22	308	34.0	59	19	AAW61322	Mutant BCL-XL/BCL-
23	159	17.6	56	21	AAW02251	Human secreted pro
24	133	14.7	26	21	AAW96321	Mammalian Bad Bcl-
25	133	14.7	26	21	AAW70371	BAD BH3 consensus
26	132	14.6	25	23	ABP56161	PRC-interacting T
27	132	14.6	25	23	ABG78484	Mutant Bcl2 compet
28	132	14.6	25	23	AAU78610	Mutant Bcl2 compet
29	129	14.3	25	23	ABG78490	Mutant Bcl2 compet
30	129	14.3	25	23	AAU78617	Mutant Bcl2 compet
31	128	14.1	25	23	ABG78488	Mutant Bcl2 compet
32	128	14.1	25	23	ABG78489	Mutant Bcl2 compet
33	128	14.1	25	23	AAU78615	Mutant Bcl2 compet
34	128	14.1	25	23	AAU78616	Mutant Bcl2 compet
35	127	14.0	24	23	AAU78627	Mutant Bcl2 compet
36	127	14.0	25	23	ABG78486	Mutant Bcl2 compet
37	127	14.0	25	23	ABG78493	Mutant Bcl2 compet
38	127	14.0	25	23	ABG78497	Mutant Bcl2 compet
39	127	14.0	25	23	AAU78612	Mutant Bcl2 compet
40	127	14.0	25	23	AAU78620	Mutant Bcl2 compet
41	127	14.0	25	23	AAU78624	Mutant Bcl2 compet
42	126	13.9	25	23	ABG78485	Mutant Bcl2 compet
43	126	13.9	25	23	ABG78492	Mutant Bcl2 compet
44	126	13.9	25	23	AAU78611	Mutant Bcl2 compet
45	126	13.9	25	23	AAU78619	Mutant Bcl2 compet

ALIGNMENTS

RESULT 1	AAW55779	standard; Protein; 168 AA.
ID	AAW55779	
AC	AAW55779	
DT	17-JUL-1998	(first entry)
DE	Human Bcl-XL/Bcl-2 associated death promoting polypeptide.	
KM	Human; Bcl-XL/Bcl-2 associated death promoting polypeptide; Bad;	
KW	programmed cell death; apoptosis.	
OS	Homo sapiens.	
PN	MO9812328-A2.	
PD	26-MAR-1998.	
PF	18-SEP-1997;	97WO-US16991.
PR	20-SEP-1996;	96US-0717123.
PA	(IDUN-) IDUN PHARM INC.	
PI	Horne WA, Oltersdorf T;	
DR	WPI: 1998-217767/19.	
DR	N-PSDB; AAV25877.	
PT	Bad gene mediating apoptosis - used to develop products for treating	
PT	e.g. neurodegenerative disease, cancers or autoimmune disease	

XX Claim 8; Fig 1; 41pp; English.

CC The present sequence is the human Bcl-XL/Bcl-2 associated
 CC death promoting polypeptide, Bad, the binding of which to Bcl-XL
 CC results in the induction of programmed cell death, i.e. apoptosis.
 CC Bad can be used in screening assays for compounds to treat or
 CC prevent diseases characterised by apoptotic cell death, such as
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.
 CC aplastic anaemia and ischaemic injury including myocardial
 CC infarction, stroke and reperfusion injury. Assays can also be
 CC used to obtain apoptosis enhancing compounds to treat or prevent
 CC diseases characterised by the loss of apoptotic cell death, such as
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated
 CC glomerulonephritis and viral infections, e.g. herpesvirus,
 CC poxvirus or adenovirus infection. Bad can also be used for
 CC detection and diagnosis.

XX Sequence 168 AA;

Query Match 100.0%; Score 905; DB 19; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.3e-87;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEPSEOEEDSSAERGLGPPAGDPSGSGKHROAPGLMDASHQOEPTSSSH 60
 DB 1 MFQIPEPSEOEEDSSAERGLGPPAGDPSGSGKHROAPGLMDASHQOEPTSSSH 60
 QY 61 HGAGAVEIRSRHSSYPAGTEDEGMEEPSPFRGRSRAPNLMQAORYGRELRMSDE 120
 DB 61 HGAGAVEIRSRHSSYPAGTEDEGMEEPSPFRGRSRAPNLMQAORYGRELRMSDE 120
 QY 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFGQSWMDNLGRGSSAPSQ 168
 DB 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFGQSWMDNLGRGSSAPSQ 168

RESULT 2

AAB13512 ID AAB13512 standard; protein; 168 AA.

XX AAB13512;

DT 02-NOV-2000 (first entry)

DE Human cell proliferation protein APOP-1.

XX Human; cell proliferation; APOP-1; cancer; inflammation; infection;
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.

OS Homo sapiens.

PN US6080847-A.

PD 27-JUN-2000.

PF 04-DEC-1997; 97US-0985335.

PR 04-DEC-1997; 97US-0985335.

PA (INCYTE) INCYTE PHARM INC.

PI Corley NC, Hillman JL, Yue H, Lal P, Shah P;

XX MPI; 2000-451230/39.

DR N-PSDB; AAA63332.

PT Novel polynucleotide and polypeptide sequences of proteins associated
 with cell proliferation for diagnosis, prevention and treatment of e.g.
 PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease -

XX Example 8; Fig 1; 58pp; English.

CC The present sequence is the human APOP-1 protein. This protein, which
 CC shares structural and chemical homology with Bcl-2, is involved in cell
 CC proliferation. Its coding sequence was isolated by screening a synovial
 CC tissue cDNA library using a computer search for amino acid sequence
 CC alignments. The gene and protein can be used in the treatment of various
 CC cancers, disorders with associated inflammation such as Addison's
 CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
 CC of cancer, haemodialysis and extracorporeal circulation, infections,
 CC trauma, disorders with associated apoptosis including AIDS and other
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
 CC such as myocardial infarction, and wasting diseases including cachexia.

XX Sequence 168 AA;

Query Match 100.0%; Score 905; DB 21; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.3e-87;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEPSEOEEDSSAERGLGPPAGDPSGSGKHROAPGLMDASHQOEPTSSSH 60
 DB 1 MFQIPEPSEOEEDSSAERGLGPPAGDPSGSGKHROAPGLMDASHQOEPTSSSH 60
 QY 61 HGAGAVEIRSRHSSYPAGTEDEGMEEPSPFRGRSRAPNLMQAORYGRELRMSDE 120
 DB 61 HGAGAVEIRSRHSSYPAGTEDEGMEEPSPFRGRSRAPNLMQAORYGRELRMSDE 120
 QY 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFGQSWMDNLGRGSSAPSQ 168
 DB 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFGQSWMDNLGRGSSAPSQ 168

RESULT 3

AAB70368 ID AAB70368 standard; protein; 168 AA.

XX AAB70368;

DT 02-MAY-2001 (first entry)

DE Human BAD mutant amino acid sequence SEQ ID NO:1.

XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
 KW cyostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.

OS Homo sapiens.

OS Synthetic.

PN WO200110888-A1.

PD 15-FEB-2001.

PF 30-MAY-2000; 2000WO-US11864.

PR 28-MAY-1999; 99US-0136783.

PA (APOP-) APOPTOSIS TECHNOLOGY INC.

XX Zhou X;

DR	PPI; 2001-138734/14.
XX	
PT	New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
PT	useful for screening for candidate compounds which induce or inhibit
PT	apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
XX	Ser113 -
PS	
CC	Claim 1, Page 147, 157pp; English.
XX	
CC	The present invention describes an isolated or synthetic polypeptide
CC	(I) comprising a less than full length amino acid sequence of a mutant
CC	Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
CC	fragment, which contains amino acid substitutions at Ser118 of a human
CC	BAD. Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
CC	BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
CC	neurotropic, antischismic, vulnerary, cytostatic, antiviral,
CC	antiatheritic, antiinflammatory and immunosuppressive activities, and
CC	can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
CC	polynucleotides can be used for screening candidate compounds and drugs
CC	for activity that promote cell survival or apoptosis. Other uses include
CC	inducing or inhibiting apoptosis in a cell. Candidate compounds
CC	identified and (mutant) BAD polypeptides are useful in treating
CC	immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
CC	death, reperfusion cell death, wound healing, cancer, viral infections,
CC	lymphoproliferative conditions, arthritis, infertility, inflammation and
CC	autoimmune diseases. The present sequence represents a specifically
CC	claimed human BAD mutant amino acid sequence from the present invention.
XX	
SQ	Sequence 168 AA;
Query Match	100.0%; Score 905; DB 22; Length 168;
Best Local Similarity	100.0%; Pred. No. 1.3e-87;
Matches 168; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 MFQIDPEPSEDESDSSAERGLCPSPAGDPSGSGKHHRQAFLMDASHOQPRTSSSH 60
DB	1 MFQIREFESBEDSSAERGICLPSPAGDPSSGSGHHHQAFLMDASHOQEPRTSSSH 60
OY	61 HGGAGAVEIRSHHSYPACTEDDECGMEESPFRGRSRSAAPNLMAORYGRLRMSDE 120
DB	61 HGGAGAVEIRSHRSYPACTEDEDGMEESPFRGRSRSAAPNLMAORYGRLRMSDE 120
OY	121 FVDSFKKGLPRPKSAGTATQMOSSTWTFVFGSWWRNLTGRGSSAFSQ 168
DB	121 FVDSFKKGLPRPKSAGTATQMOSSTWTFVFGSWWRNLTGRGSSAFSQ 168
RESULT 4	
AAB48287	
ID	AAB48287 standard; protein; 168 AA.
XX	
AC	AAB48287;
XX	
DT	02-APR-2001 (first entry)
XX	
DE	Human Bad protein.
XX	
XX	
OS	Homo sapiens.
PN	MO200075184-A1.
PD	14-DEC-2000.
XX	
PF	05-JUN-2000; 2000WO-US15449.
XX	
PR	04-JUN-1999; 99US-0137494.
XX	
DA	(UYVA) UNIV YALE.
XX	

Pt	Zhang H, Tsvetkov LM, Kondo T;
XX	wpi; 2001-061703/07.
DR	N-Psdb; AAC84599.
XX	
Pt	Modulating polypeptide levels in a cell, diagnosing and treating tumor,
Pt	involves altering levels of proteins such as S-phase kinase associated
Pt	proteins 1, 2 and cullin/CDC3 proteins -
XX	
PS	Claim 5; Page 102-103; 162pp; English.
XX	
CC	The invention relates to methods of altering the polypeptide levels in a
CC	cell, using proteins selected from S-phase kinase associated proteins 1
CC	and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC	cullin/ CDC3 family of proteins). The method is useful for altering the
CC	level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC	polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC	detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC	that modulate interactions between Skp and target proteins are useful for
CC	treating tumours.
SQ	
SQ	Sequence 168 AA;
Query Match	100.0%; Score 905; DB 22; Length 168;
Best Local Similarity	100.0%; Pred. No. 1.3e-87;
Matches 168; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Oy	1 MFOLPEFPSSQEDSSAERGLGPPADGSGSGKHHROAPGLMDASHOQOPTSSSH 60
Dd	1 MFOIPEFPSPSQEDBSSAERGLGPSPADGDGPGSGKHROAPGLMDASHOQOPTSSSH 60
Oy	61 HGAGAVFIRSRHSSYPAGTDEDBCGMGESPFRGRSSAPPNLMAAQYRGELRMSDE 120
Dd	61 HGGAIVAIRSRHSSYPAGTDEDBCGMGESPPFRGRSSAPPNLMAAQYRGELRMSBB 120
Oy	121 FVDSFFKGLPRPKSAGTATOMRGSSWTRVCSMWDRNLGRSSASPQ 168
Dd	121 FVDSFFKGLPRPKSAGTATOMRGSSWTRVFQSWMDRLNIGRSSASPO 168
RESULT 5	
AAG67688	ID AAG67688 standard; Protein, 168 AA.
XX	
AC	AAG67688;
XX	
DT	26-NOV-2001 (first entry)
XX	
De	Amino acid sequence of protein associated with cell proliferation-1.
XX	
KW	Human; cell proliferation; APOB-1; APOB-2; APOB-3; apoptosis; cancer;
KW	brain cancer; breast cancer; Alzheimer's disease; Parkinson's disease;
KW	inflammation; allergy; gout; osteoarthritis; bronchitis.
XX	
OS	Homo sapiens.
XX	
FH	Key
FH	Modified-site
FT	/note= "potential casein kinase II phosphorylation site"
FT	Modified-site.
FT	/note= "potential casein kinase II phosphorylation site".
FT	Modified-site
FT	/note= "potential protein kinase C phosphorylation site"
FT	Modified-site
FT	/note= "potential casein kinase II phosphorylation site"
FT	Modified-site
FT	/note= "potential cAMP- and cGMP-dependent protein
FT	kinase phosphorylation site"
FT	Modified-site
FT	/note= "potential casein kinase C phosphorylation site"
FT	Modified-site
FT	/note= "potential casein kinase II phosphorylation site"
XX	

PN US6281334-B1.
 XX 28-AUG-2001.
 PD 30-SEP-1999; 99US-0410372.
 XX 04-DEC-1997; 97US-0985335;
 XX (INCY-) INCYTE GENOMICS INC.
 PA Hillman JL, Yue H, Lal P, Shah P, Corley NC;
 XX WPI; 2001-569961/64.
 DR N-PSDB; AAH78430.
 XX
 PT New polypeptides associated with cell proliferation, useful for
 PT preventing or treating cancer (e.g. brain cancer), a disorder
 PT associated with an increase in apoptosis (e.g. Alzheimer's disease) or
 PT inflammation (e.g. gout).
 PS Example; Fig 1A-C; 59pp; English.
 XX
 CC The present sequence represents a human protein which is associated
 CC with cell proliferation, designated APOP-1. The specification also
 CC describes APOP-2 and APOP-3. The APOP polypeptides are useful for
 CC diagnosing, preventing or treating disorders associated with abnormal
 CC cell proliferation and apoptosis. The polypeptides and composition are
 CC particularly useful for treating or preventing cancer (e.g. brain or
 CC breast cancer), a disorder associated with an increase in apoptosis
 CC (e.g. Alzheimer's disease or Parkinson's disease) or inflammation
 CC (e.g. allergies, gout, osteoarthritis or bronchitis).
 CC
 SQ Sequence 168 AA;

Query Match 100.0%; Score 905; DB 22; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.3e-87;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFQIPEPSPSEQEDSSAERGLGSPAGDPSGSGKHROAPGLMDASHOQEOPTSSSH 60
 DB 1 MFQIPEPSPSEQEDSSAERGLGSPAGDPSGSGKHROAPGLMDASHOQEOPTSSSH 60
 QY 61 HGGAGAVEIRSRHSSTYAGTDEDDGMEEPSPFGRSRSAAPNLMAAQRGRELRRMSDE 120
 DB 61 HGGAGAVEIRSRHSSTYAGTDEDDGMEEPSPFGRSRSAAPNLMAAQRGRELRRMSDE 120
 QY 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFOQSWMDNLGRGSSAPSQ 168
 DB 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFOQSWMDNLGRGSSAPSQ 168

RESULT 6
 ABR39081
 ID ABR39081 standard; Protein; 168 AA.
 XX ABR39081;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Human BAD protein SEQ ID NO:2.
 XX
 KW Human; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
 KW virucide; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO2003012049-A2.
 PD 13-FEB-2003.
 XX
 PF 31-JUL-2002; 2002WO-US24177.
 XX
 PR 31-JUL-2001; 2001US-308929P.

XX (UYCH-) UNIV CHICAGO.
 PA Munger J, Roizman B;
 XX WPI; 2003-248168/24.
 DR N-PSDB; ABZ81200.
 XX
 PT Inducing apoptosis in a cell infected with herpes simplex virus, HSV,
 PT by administering to the cell, a composition comprising an agent that
 PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
 XX
 Claim 15; Page 166-167; 192pp; English.
 XX
 CC The present invention describes a method (M1) for inducing apoptosis in
 CC a cell infected with herpes simplex virus (HSV), which comprises
 CC administering to the cell, a composition having an agent that inhibits
 CC phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also
 CC described is a method (M2) for treating a patient infected with HSV, by
 CC administering to the patient, a composition comprising a peptide
 CC comprising a sequence of 4-100 continuous amino acids of a 168 residue
 CC amino acid sequence (see ABR39081), where the peptide comprises ser112,
 CC ser135, or ser155, or their combinations. BAD has virucide activity.
 CC M1 is useful for inducing apoptosis in a cell infected with HSV, where
 CC the cell is in a human. M2 is useful for treating a patient infected
 CC with HSV. The present sequence represents human BAD, which is used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 168 AA;

Query Match 100.0%; Score 905; DB 24; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.3e-87;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFQIPEPSPSEQEDSSAERGLGSPAGDPSGSGKHROAPGLMDASHOQEOPTSSSH 60
 DB 1 MFQIPEPSPSEQEDSSAERGLGSPAGDPSGSGKHROAPGLMDASHOQEOPTSSSH 60
 QY 61 HGGAGAVEIRSRHSSTYAGTDEDDGMEEPSPFGRSRSAAPNLMAAQRGRELRRMSDE 120
 DB 61 HGGAGAVEIRSRHSSTYAGTDEDDGMEEPSPFGRSRSAAPNLMAAQRGRELRRMSDE 120
 QY 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFOQSWMDNLGRGSSAPSQ 168
 DB 121 FVDSFKKGLPRPKSAGTATQWRQSSSWTRVFOQSWMDNLGRGSSAPSQ 168

RESULT 7
 ABP41630
 ID ABP41630 standard; Protein; 201 AA.
 XX ABP41630;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HCE4K28, SEQ ID NO:2762.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 PD 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.
PF
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR N-PSDB; ABO54707.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX
PS Claim 11; SEQ ID NO 2762; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABO54131-ABO56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_poc_sequences.
XX
SQ Sequence 201 AA;
Query Match 95.5%; Score 864; DB 23; Length 201;
Best Local Similarity 98.2%; Pred. No. 3.5e-83;
Matches 160; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MFQIEPFESEBDDSSAERGLGPPADGPGSGGKHHRAQGLMDASHOEOPTSSH 60
DB 9 MFQIEPFESEBDDSSAERGLGPPADGPGSGGKHHRAQGLMDASHOEOPTSSH 68
QY 61 HCGAGAVEIRSRHSSYPACTEDDEGMEGEPSPFRGRSRAPNLTMAAORYGRLRMSDE 120
DB 69 HCGAGAVEIRSRHSSYPACTEDDEGMEGEPSPFRGRSRAPNLTMAAORYGRLRMSDE 128
QY 121 FVDSFKKGLPRPKSAGTATQKROSSWTRVFQSWMDRNLGRGSSAPSQ 163
DB 129 FVDSFKKGLPRPKSAGTATQKROSSWTRVFQSWMDRNLGRGSSAPSQ 171
RESULT 8
AAW32476
ID AAW32476 standard; Protein; 166 AA.
XX
AC AAW32476;

XX 15-JAN-1998 (first entry)
DT
XX
XX BbC6 protein for regulating cell death.
DE
XX BbC6 gene; cell death; cell cycle; Bcl2; human.
XX
XX Homo sapiens.
OS
XX
PN US5663316-A.
XX
PD 02-SEP-1997.
XX
PF 18-JUN-1996; 96US-0665617.
XX
PR 18-JUN-1996; 96US-0665617.
XX
XX (CLON-) CLONTECH LAB INC.
XX
XX Xudong Y;
XX
DR WPI; 1997-447980/41.
DR N-PSDB; AAT91561.
XX
PT Isolated BbC6 gene - encodes a protein that regulates cell death
PT through interaction with Bcl-2
XX
PS Claim 1; Column 11-12; 7pp; English.
XX
XX The present sequence represents a protein of 166 amino acids. The
CC sequence is disclosed as being a protein called BbC6 which regulates
CC cell death through interaction with Bcl-2. The DNA may be used for the
CC production of the recombinant protein, which can be used in unspecified
CC therapeutic or diagnostic procedures, as a molecular weight marker, and
CC to raise antibodies that can be used in unspecified diagnostic or
CC therapeutic applications and to reduce or eliminate the biological
CC activity of the BbC6 protein in vivo.
XX
SQ Sequence 166 AA;
Query Match 83.0%; Score 751; DB 18; Length 166;
Best Local Similarity 84.0%; Pred. No. 2.5e-71;
Matches 147; Conservative 3; Mismatches 9; Indels 16; Gaps 3;
QY 1 MFQIEPFESEBDDSSAERGLGPPADGPGSGGKHHRAQGLMDASHOEOPTSSH 53
DB 1 MFQIEPFESEBDDSSAERGLGPPADGPGSGGKHHRAQGLMDASHOEOPTSSH 51
QY 54 OPTSSHHGAGAVEIRSRHSSYPACTEDDEGMEGEPSPFRGRSRAPNLTMAAORYGRL 113
DB 52 OPTSSHHGAGAVEIRSRHSSYPACTEDDEGMEGEPSPFRGRSRAPNLTMAAORYGRL 111
QY 114 LRMSDEFVDSFKKGLPRPKSAGTATQKROSSWTRVFQSWMDRNLGRGSSAPSQ 168
DB 112 LRMSDEFVDSFKKGLPRPKSAGTATQKROSSWTRVFQSWMDRNLGRGSSAPSQ 166
RESULT 9
AAB70370
ID AAB70370 standard; Protein; 162 AA.
XX
AC AAB70370;
XX
DT 02-MAY-2001 (first entry)
XX
XX Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
XX
XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
KW immunostimulant; neuroprotective; nootropic; antischismatic; vulnery;
KW cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;
KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
KW immunodeficiency disease; neurodegenerative disease; viral infection;
KW ischaemic cell death; reperfusion cell death; arthritis; infectivity;

RESULT 11

AAM61315 standard; Protein; 204 AA.

AAM61315;

07-OCT-1998 (first entry)

Murine BCL-XL/BCL-2 associated cell death regulator.

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.

Mus sp.

M09817682-A1.

30-APR-1998.

17-OCT-1997; 97MO-US19175.

18-OCT-1996; 96US-0733505.

(UNIW) UNIV WASHINGTON.

Koremeier SJ;

WPI; 1998-261422/23.

N-PSDB; AAV27833.

New mutant BAD polypeptide with phosphorylatable serine replaced - useful for, e.g. treating reduced apoptosis such as in cancer or viral infection

Claim 1; Fig 10; 95pp; English.

The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

Sequence 204 AA;

Query Match 71.7%; Score 649; DB 19; Length 204;

Best Local Similarity 75.6%; Pred. No. 2e-60; Mismatches 23; Indels 6; Gaps 3;

Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

1 MFQIPPEPSROEBSAERGIGPSPADGSGSGKXKRAAGLLMDASHOQEPQTSSH 60
 43 MFQIPPEPSROEBSAERGIGPSPADGSGSGKXKRAAGLLMDASHOQEPQTSSH 97
 61 HGGAGAVEIRSHSSYPAGTEDEGMEGEPSPFGRGRSAPPNLMQAORYGRIELRMDS 120

98 HGGAGAVEIRSHSSYPAGTEDEGMEGEBELPPFRGRSAPPNLMQAORYGRIELRMDS 157
 121 FVDSFKKGLPRPKSACTATQWRSSSWTRVRSQWMDRLGCGSSAPSQ 168
 158 FEGSF-KGLPRPKSAGTATQWRSSAGWTRIIQSWMDRLGCGGSTPSQ 204

RESULT 12

AAM58832 standard; Protein; 204 AA.

AAM58832;

23-JUL-1998 (first entry)

Murine BAD protein.

BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer; viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.

Mus sp.

M09809643-A1.

12-MAR-1998.

09-SEP-1997; 97MO-US15871.

09-SEP-1996; 96US-0707868.

(UNIW) UNIV WASHINGTON.

Koremeier SJ;

WPI; 1998-207049/18.

Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases

Claim 3; Fig 8; 61pp; English.

This sequence represents a novel serine-phosphorylated protein, BAD (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is phosphorylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator. Modulators of phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphatase, are useful for preventing/treating increased/decreased apoptosis in a cell. The increased apoptosis may result from immunodeficiency diseases, senescence, neurodegenerative disease, ischaemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infection, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. Measuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.

Sequence 204 AA;

Query Match 71.7%; Score 649; DB 19; Length 204;

Best Local Similarity 75.6%; Pred. No. 2e-60; Mismatches 23; Indels 6; Gaps 3;

Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

1 MFQIPPEPSROEBSAERGIGPSPADGSGSGKXKRAAGLLMDASHOQEPQTSSH 60
 43 MFQIPPEPSROEBSAERGIGPSPADGSGSGKXKRAAGLLMDASHOQEPQTSSH 97
 61 HGGAGAVEIRSHSSYPAGTEDEGMEGEPSPFGRGRSAPPNLMQAORYGRIELRMDS 120

Db 98 HGGAGMETSRHSSTYAGTEDEGMEBELSPFRGRSRAPNULMAQRYGRELRRMSDE 157
 QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFGSWMDNLGRGSSAPSQ 168
 Db 158 FEGSF-KGLPRPKSAGTATOMROSAGWTRIIOSWMDNLKGGSTPSQ 204

RESULT 13
 AAB70369
 ID AAB70369 standard; protein; 204 AA.
 XX
 AC AAB70369;
 XX
 DT 02-MAY-2001 (first entry)
 XX

DE Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
 XX

KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; nootropic; antischismic; vulnery;
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX

OS Mus musculus.
 OS Synthetic.
 XX

PN WO200110888-A1.
 XX

PD 15-FEB-2001.
 XX

PF 30-MAY-2000; 2000WO-US11864.
 XX

PR 28-MAY-1999; 99US-0136783.
 XX

PA (APOF-) APOPTOSIS TECHNOLOGY INC.
 XX

PI Zhou X;
 XX

DR WPI; 2001-138734/14.
 XX

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX

PS Claim 4; Page 148; 157pp; English.
 XX

CC The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC nootropic, antischismic, vulnery, cyrostatic, antiviral,
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed longer murine BAD mutant amino acid sequence from the present
 CC invention.
 XX

XX Sequence 204 AA;
 SQ

Query Match 71.7%; Score 649; DB 22; Length 204;

Best Local Similarity 75.6%; Pred. No. 2e-60;
 Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPESEQEDSSAERGLGPPAGDGPSSGKHHROAPGLMDASHQOEPTSSSH 60

Db 43 MFQIPEPESEQEDSSAERGLGPPAGDGPSSGKHHROAPGLMDASHQOEPTSSSH 97

QY 61 HGGAGAVEIRSRHSSTYAGTEDEGMEBELSPFRGRSRAPNULMAQRYGRELRRMSDE 120

Db 98 HGGAGMETSRHSSTYAGTEDEGMEBELSPFRGRSRAPNULMAQRYGRELRRMSDE 157

QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFGSWMDNLGRGSSAPSQ 168
 Db 158 FEGSF-KGLPRPKSAGTATOMROSAGWTRIIOSWMDNLKGGSTPSQ 204

RESULT 14
 ABR39082
 ID ABR39082 standard; protein; 204 AA.
 XX
 AC ABR39082;
 XX

DT 10-MAY-2003 (first entry)
 XX

DE Murine BAD protein SEQ ID NO:4.
 XX

DE Murine BAD protein SEQ ID NO:4.
 XX

KW Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
 KW virucide; infection.
 XX

KW Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
 KW virucide; infection.
 XX

OS Mus musculus.
 OS WO2003012049-A2.
 XX

PN WO2003012049-A2.
 XX

PD 13-FEB-2003.
 XX

PF 31-JUL-2002; 2002WO-US24177.
 XX

PR 31-JUL-2001; 2001US-308929P.
 XX

PA (UYCH-) UNIV CHICAGO.
 XX

PI Munger J; Roizman B;
 XX

DR WPI; 2003-248168/24.
 XX

DR N-PSDB; ABZ81201.
 XX

PT Inducing apoptosis in a cell infected with herpes simplex virus, HSV,
 PT by administering to the cell, a composition comprising an agent that
 PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3 -
 XX

PS Claim 15; Page 168; 192pp; English.
 XX

CC The present invention describes a method (M1) for inducing apoptosis in
 CC a cell infected with herpes simplex virus (HSV), which comprises
 CC administering to the cell, a composition having an agent that inhibits
 CC phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also
 CC described is a method (M2) for treating a patient infected with HSV, by
 CC administering to the patient, a composition comprising a peptide
 CC comprising a sequence of 4-100 continuous amino acids of a 168 residue
 CC amino acid sequence (see ABR39081), where the peptide comprises ser112,
 CC ser135, or ser155, or their combinations. BAD has virucide activity.
 CC M1 is useful for inducing apoptosis in a cell infected with HSV, where
 CC the cell is in a human. M2 is useful for treating a patient infected
 CC with HSV. The present sequence represents murine BAD, which is used in
 CC the exemplification of the present invention.
 XX

SQ Sequence 204 AA;
 SQ

Query Match 71.7%; Score 649; DB 24; Length 204;

Best Local Similarity 75.6%; Pred. No. 2e-60;
 Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPESEQEDSSAERGLGPPAGDGPSSGKHHROAPGLMDASHQOEPTSSSH 60


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DB      43 MFQIPFEPSEDESDASATDRGLGSLTEQDQ---GPY--LAPGLGSMNHQGRATNSH 97
QY      61 HGGAGAVEIRSRHSSYPAGTEDEDEGMEGEPSPFRGRSRAPPNLMAAQRYGRELRMSDE 120
DB      98 HGGAGAMETRSRHSSTYPAGTEDEDEGMEBELSPFRGRSRAPPNLMAAQRYGRELRMSDE 157
QY      121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFSQWMDRNLGRGSSAPSQ 168
DB      158 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWMDRNLGRGSSAPSQ 204

RESULT 15
ID      AAM61317
XX      AAM61317 standard; Protein; 204 AA.
XX      AAM61317;
XX      07-OCT-1998 (first entry)
XX      DT
XX      DE Mutant BCL-XL/BCL-2 associated cell death regulator #2.
XX      DE Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX      KM serine substituted mutant; apoptosis; cancer; viral infection.
XX      OS Mus sp.
XX      OS Synthetic.
XX      PN MO9817682-A1.
XX      PD 30-APR-1998.
XX      PF 17-OCT-1997; 97MO-US19175.
XX      PR 18-OCT-1996; 96US-0733505.
XX      PA (UNITW ) UNITV WASHINGTON.
XX      PI Koremeyer SJ;
XX      DR WPI; 1998-261422/23.
XX      DR N-PSDB; AAV27835.
XX      PT New mutant BAD polypeptide with phosphorylatable serine replaced -
XX      PT useful for, e.g. treating reduced apoptosis such as in cancer or
XX      PT viral infection
XX      PS Claim 7, Page 60; 95pp; English.
XX      PS
XX      CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX      CC death regulator) proteins, having an amino acid other than Ser at
XX      CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX      CC present sequence represents a mutant BAD protein. Also described are: (1)
XX      CC fragments of mutant BAD protein able to decrease cell viability; (2)
XX      CC fusion proteins of mutant BAD with a heterologous polypeptide that
XX      CC increases intracellular delivery. Mutant BAD proteins are used to treat
XX      CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX      CC viral infection, lymphoproliferation, arthritis, infertility,
XX      CC inflammation and autoimmune disease. Polynucleotide sequences encoding
XX      CC mutant BAD-proteins can be used similarly by gene therapy or to produce
XX      CC transgenic animals for use as disease models or in drug screening. BAD
XX      CC proteins phosphorylated at specified Ser are used to screen for enhancers
XX      CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX      CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX      CC aging or ischemic cell death. The apoptotic status of cells is
XX      CC determined by measuring relative amounts of phosphorylated and non-
XX      CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX      CC greater death-promoting activity than wild-type BAD which can become
XX      CC phosphorylated on the specified Ser, forming a product that does not
XX      CC heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX      CC proteins in the cytosol, thus promoting cell survival. The mutants with
XX      CC Ser substituted cannot bind 14-3-3.

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SQ      Sequence      204 AA;
Query Match      71.4%; Score 646; DB 19; Length 204;
Best Local Similarity 75.0%; Pred. No. 4,2e-60;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;
QY      1 MFQIPFEPSEDESDSSAERGIGPSPADGPGSGSKHROAPGLMDASHOQEQPTSSSH 60
DB      43 MFQIPFEPSEDESDASATDRGLGSLTEQDQ---GPY--LAPGLGSMNHQGRATNSH 97
DB      61 HGGAGAVEIRSRHSSYPAGTEDEDEGMEGEPSPFRGRSRAPPNLMAAQRYGRELRMSDE 120
DB      98 HGGAGAMETRSRHSSTYPAGTEDEDEGMEBELSPFRGRSRAPPNLMAAQRYGRELRMSDE 157
QY      121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFSQWMDRNLGRGSSAPSQ 168
DB      158 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWMDRNLGRGSSAPSQ 204

```

Search completed: December 29, 2003, 23:30:51
 Job time : 77 secs

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XX WPI: 2003-248168/24.
 DR P-PSDB; ABR39081.
 XX
 PT Inducing apoptosis in a cell infected with herpes simplex virus, HSV,
 PT by administering to the cell, a composition comprising an agent that
 PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
 XX
 PS Disclosure; Page 165-166; 192pp; English.
 XX
 CC The present invention describes a method (M1) for inducing apoptosis in
 CC a cell infected with herpes simplex virus (HSV), which comprises
 CC administering to the cell, a composition having an agent that inhibits
 CC phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also
 CC described is a method (M2) for treating a patient infected with HSV, by
 CC administering to the patient, a composition comprising a peptide
 CC comprising a sequence of 4-100 continuous amino acids of a 168 residue
 CC amino acid sequence (see ABR39081), where the peptide comprises ser12,
 CC ser135, or ser155, or their combinations. BAD has virucide activity.
 CC M1 is useful for inducing apoptosis in a cell infected with HSV, where
 CC the cell is in a human. M2 is useful for treating a patient infected
 CC with HSV. The present sequence encodes human BAD, which is given in the
 CC exemplification of the present invention.
 CC
 XX Sequence 945 BP; 185 A; 294 C; 309 G; 157 T; 0 other;
 SQ
 Query Match 99.9%; Score 945; DB 25; Length 945;
 Best Local Similarity 100.0%; Pred. No. 6.7e-226;
 Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGCTAGAGGCGCCGGGTCAAGGGGCTTCAGATTCGGGCTTGGGCCAGAGCATGTTCCAG 60
 DB 1 GGGGCTAGAGGCGCCGGGTCAAGGGGCTTCAGATTCGGGCTTGGGCCAGAGCATGTTCCAG 60
 QY 61 ATCCAGAGTTTGAAGCCAGATGAGCAGAGAAAGCTTCAGCTTCGCGAAGAGGGGCTGGGC 120
 DB 61 ATCCAGAGTTTGAAGCCAGATGAGCAGAGAAAGCTTCAGCTTCGCGAAGAGGGGCTGGGC 120
 QY 121 CCCAGCCCCGAGAGGGGAGGGGCTCAGGCTCCGGGCAAGCATCATCGCAGAGGCCCAAGC 180
 DB 121 CCCAGCCCCGAGAGGGGAGGGGCTCAGGCTCCGGGCAAGCATCATCGCAGAGGCCCAAGC 180
 QY 181 CTCCTGTGGAGCGCCAGTCACCAAGAGAGAGCCAAACAGAGAGAGCCATCATGAGAGC 240
 DB 181 CTCCTGTGGAGCGCCAGTCACCAAGAGAGAGCCAAACAGAGAGAGCCATCATGAGAGC 240
 QY 241 GCTGGGGCTGTGGAGATCCGAGTGCACAGCTCTTACCCCGGGGAGCGAGAGACAC 300
 DB 241 GCTGGGGCTGTGGAGATCCGAGTGCACAGCTCTTACCCCGGGGAGCGAGAGACAC 300
 QY 301 GAAAGGATGGGGAGAGAGCCGAGCCCTTGGGGGCGCTGGCGCTGGCCGCCCCCAAC 360
 DB 301 GAAAGGATGGGGAGAGAGCCGAGCCCTTGGGGGCGCTGGCGCTGGCCGCCCCCAAC 360
 QY 361 CTCCTGGAGAGACAGCGCTATGCGCGAGCTCCGAGAGATGAGTGAAGTTGTGAC 420
 DB 361 CTCCTGGAGAGACAGCGCTATGCGCGAGCTCCGAGAGATGAGTGAAGTTGTGAC 420
 QY 421 TCCTTTAAGAAAGGACTTCTCGCCGAGAGCGGGCAGACAGCAACCAAGTCGGCA 480
 DB 421 TCCTTTAAGAAAGGACTTCTCGCCGAGAGCGGGCAGACAGCAACCAAGTCGGCA 480
 QY 481 AGCTCCAGCTGAGACGCGAGTCTTCAGATTCCTGGTGGATTCGGAATTTGGGAGGAAAC 540
 DB 481 AGCTCCAGCTGAGACGCGAGTCTTCAGATTCCTGGTGGATTCGGAATTTGGGAGGAAAC 540
 QY 541 TCCGCCCCCTCCAGATGCTTCGATCCACATCCGGAATCCACCCGTTCCATTGGCCT 600
 DB 541 TCCGCCCCCTCCAGATGCTTCGATCCACATCCGGAATCCACCCGTTCCATTGGCCT 600
 QY 601 GGGGAGCCATTTTGAATATGGAGAGAGTAACTTCTTCAGGCTTATGCAAAAAGAGAT 660
 DB 601 GGGGAGCCATTTTGAATATGGAGAGAGTAACTTCTTCAGGCTTATGCAAAAAGAGAT 660

QY 661 CCGTGTGTATTCCTTTGAGAGGAGGTTGACCCAGATTCCTTCGGTGTGTGAAGCC 720
 DB 661 CCGTGTGTATTCCTTTGAGAGGAGGTTGACCCAGATTCCTTCGGTGTGTGAAGCC 720
 QY 721 ACGGAGGTTGTGTCCATCGGAAGTTTGGGTTTCCGCCACAGCCCGGAGAGTGGCT 780
 DB 721 ACGGAGGTTGTGTCCATCGGAAGTTTGGGTTTCCGCCACAGCCCGGAGAGTGGCT 780
 QY 781 CCGTGGCCCGCCCTCAGGTTCCGGGGTTTCCCGCAGGCGCTGCTAAGTACGAGCC 840
 DB 781 CCGTGGCCCGCCCTCAGGTTCCGGGGTTTCCCGCAGGCGCTGCTAAGTACGAGCC 840
 QY 841 AGGTTTAACGTTGTGTACCGGAGCCGAGCCCGCGATGCTTGGGGGCGGTGATCA 900
 DB 841 AGGTTTAACGTTGTGTGTACCGGAGCCGAGCCCGCGATGCTTGGGGGCGGTGATCA 900
 QY 901 GTACCAATGTATTAAGCCCGCGTGTGTGCCAAAAA 945
 DB 901 GTACCAATGTATTAAGCCCGCGTGTGTGCCAAAAA 945
 RESULT 2
 ID AAV25877 standard; cDNA; 946 BP.
 XX AAV25877;
 AC AAV25877;
 XX
 DT 17-JUL-1998 (first entry)
 XX
 XX cDNA for human Bcl-xL/Bcl-2 associated death promoting polypeptide.
 DE Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;
 KW programmed cell death; apoptosis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 52..558
 FT /*tag= a
 FT /product= Bad
 FT
 XX
 PN W09812328-A2.
 XX
 PD 26-MAR-1998.
 XX
 PF 18-SEP-1997; 97WO-US16991.
 XX
 PR 20-SEP-1996; 96US-0717123.
 XX
 PA (IDUN-) IDUN PHARM INC.
 XX
 PI Horne WA, Oltersdorf T;
 XX
 XX WPI: 1998-217267/19.
 DR P-PSDB; AAW55779.
 XX
 PT Bad gene mediating apoptosis - used to develop products for treating
 PT e.g. neurodegenerative disease, cancers or autoimmune disease
 XX
 PS Claim 2; Fig 1; 41pp; English.
 XX
 CC The present sequence encodes the human Bcl-xL/Bcl-2 associated
 CC death promoting polypeptide, Bad, the binding of which to Bcl-xL
 CC results in the induction of programmed cell death, i.e. apoptosis.
 CC Bad can be used in screening assays for compounds to treat or
 CC prevent diseases characterised by apoptotic cell death, such as
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.
 CC aplastic anaemia and ischaemic injury including myocardial
 CC infarction, stroke and reperfusion injury. Assays can also be
 CC used to obtain apoptosis enhancing compounds to treat or prevent

CC diseases characterised by the loss of apoptotic cell death, such as
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated
 CC glomerulonephritis and viral infections, e.g. herpesvirus,
 CC poxvirus or adenovirus infection. Bad can also be used for
 CC detection and diagnosis.

XX Sequence 946 BP; 186 A; 295 C; 309 G; 156 T; 0 other;

Query Match 99.7%; Score 942.8; DB 19; Length 946;

Best Local Similarity 99.8%; Pred. No. 2.4e-225;

Matches 944; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 GGGCTAGGGCGCCGGGTGAGGGGCTTCAGATCGGGCTTTGGGCCCAAGCATGTTCCAG 60
DB 1 GGGCTAGGGCGCCGGGTGAGGGGCTTCAGATCGGGCTTTGGGCCCAAGCATGTTCCAG 60
QY 61 ATCCAGAGTTTGAGCCCGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 120
DB 61 ATCCAGAGTTTGAGCCCGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 120
QY 121 CCCAGCCCCGAGGGGAGCGGGCTTCAGAGCTCCGGCAAGCATATCGAGGCCCAAGGC 180
DB 121 CCCAGCCCCGAGGGGAGCGGGCTTCAGAGCTCCGGCAAGCATATCGAGGCCCAAGGC 180
QY 181 CTCTGTGGGAGCGCAGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 240
DB 181 CTCTGTGGGAGCGCAGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 240
QY 241 GCTGGGGCTGTGAGATCCGAGTCCGACAGCTCTTACCCCGGGGAGCGAGAGCAGC 300
DB 241 GCTGGGGCTGTGAGATCCGAGTCCGACAGCTCTTACCCCGGGGAGCGAGAGCAGC 300
QY 301 GAAGGAGATGGGAGGAGAGCGCCCTTCGGGGCGGCTCCGGCGGGGCGCCCGCCCAAC 360
DB 301 GAAGGAGATGGGAGGAGAGCGCCCTTCGGGGCGGCTCCGGCGGGGCGCCCGCCCAAC 360
QY 361 CTCTGGGAGCAGCAGCGCTATGCGCGAGCTCCGAGAGTATGACAGATTTGTGAC 420
DB 361 CTCTGGGAGCAGCAGCGCTATGCGCGAGCTCCGAGAGTATGACAGATTTGTGAC 420
QY 421 TCCTTTAAGAGAGCACTTCTGCGCCGAAAGCGGGGAGCAGCAAGCAAGTGGCGCA 480
DB 421 TCCTTTAAGAGAGCACTTCTGCGCCGAAAGCGGGGAGCAGCAAGCAAGTGGCGCA 480
QY 481 AGCTCAGCTGAGCGGAGCTTTCAGTCTGTGGGATCGGAATCTTGGGCGAGGAAAGC 540
DB 481 AGCTCAGCTGAGCGGAGCTTTCAGTCTGTGGGATCGGAATCTTGGGCGAGGAAAGC 540
QY 541 TCCGCCCCCTCCAGTGAACCTTCGGTCCATCCGAAATCCAGCCGTTCCATTGCCCT 600
DB 541 TCCGCCCCCTCCAGTGAACCTTCGGTCCATCCGAAATCCAGCCGTTCCATTGCCCT 600
QY 601 GGGCAGCAATTTGAAATATGAGAGAGTAAAGTTCCTTCAAGGCTATGCAAAAGAGAT 660
DB 601 GGGCAGCAATTTGAAATATGAGAGAGTAAAGTTCCTTCAAGGCTATGCAAAAGAGAT 660
QY 661 CGGTCGTATCTTGAAGAGGAGGTTGACCAATTCCTTCGGGTGTGTGAAGC 720
DB 661 CGGTCGTATCTTGAAGAGGAGGTTGACCAATTCCTTCGGGTGTGTGAAGC 720
QY 721 ACGGAGGTTGATCCATCGAAGTTTGGTTTCCGCCACAGCCCGGAGATGAGCT 780
DB 721 ACGGAGGTTGATCCATCGAAGTTTGGTTTCCGCCACAGCCCGGAGATGAGCT 780
QY 781 CCGTGGCCCCCGCTCAGAGTTCCGGGGTTTCCCGAGGAGGCTGAGTAAAGAGC 840
DB 781 CCGTGGCCCCCGCTCAGAGTTCCGGGGTTTCCCGAGGAGGCTGAGTAAAGAGC 840
QY 841 AGGTTTAAACGTTGTGACCGGAGCCGAGGCCCGCGAGATCCCTGGGGGGCGGTATCA 900
DB 841 AGGTTTAAACGTTGTGACCGGAGCCGAGGCCCGCGAGATCCCTGGGGGGCGGTATCA 900

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QY 901 GTACCAATGTTAATPAAGCCCGGTGTGTGCCCAAAAAAAAAAAAA 946
 DB 901 GTACCAATGTTAATPAAGCCCGGTGTGTGCCCAAAAAAAAAAAAA 946

RESULT 3

AAA63332 standard; cDNA; 1105 BP.

AAA63332;

02-NOV-2000 (first entry)

Human cell proliferation protein APOB-1 coding sequence.

Human; cell proliferation; APOB-1; cancer; inflammation; infection;
 trauma; neurodegenerative disease; ischaemic injury; wasting disease; ss.

Homo sapiens.

Key Location/Qualifiers

CDS /tag= a /product= "APOB-1"

US6080847-A.

27-JUN-2000.

04-DEC-1997; 97US-0985335.

04-DEC-1997; 97US-0985335.

(INCYTE) INCYTE PHARM INC.

Corley NC, Hillman JL, Yue H, Lal P, Shah P,

WPI; 2000-451230/39.

P-PSDB; AAB13512.

Novel polynucleotide and polypeptide sequences of proteins associated
 with cell proliferation for diagnosis, prevention and treatment of e.g.
 cancer, acquired immunodeficiency syndrome, and Parkinson's disease -

Example 5; Fig 1; 58pp; English.

The present sequence is the human APOB-1 coding sequence. Its protein,
 which shares structural and chemical homology with Bcl-2, is involved in
 cell proliferation. The sequence was isolated by screening a synovial
 tissue cDNA library using a computer search for amino acid sequence
 alignments. The gene and protein can be used in the treatment of various
 cancers, disorders with associated inflammation such as Addison's
 disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
 atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,
 emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel
 syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,
 myocardial or pericardial inflammation, osteoporosis, rheumatoid
 arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
 of cancer, haemodialysis and extracorporeal circulation, infections,
 trauma, disorders with associated apoptosis including AIDS and other
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases
 such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
 such as myocardial infarction, and wasting diseases including cachexia.

Sequence 1105 BP; 209 A; 368 C; 352 G; 176 T; 0 other;

Query Match 88.8%; Score 840.4; DB 21; Length 1105;

Best Local Similarity 97.9%; Pred. No. 8.3e-200;

Matches 883; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

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QY 43 GCCCAGAGCATGTTCCAGATCCAGAGTTTGAAGCCGAGTGAAGCAAGCAAGCAAGCAAGCA 102
DB 205 GCCCAGAGCATGTTCCAGATCCAGAGTTTGAAGCCGAGTGAAGCAAGCAAGCAAGCAAGCA 264

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QY	103	GCAGAGAGGGGCGTGGGCGCCAGCCCGCAGGGAGCGGGCCCTCAGGCTCTCCGGCAAGCAT	162
Db	265	GCAGAGAGGGGCGTGGGCGCCAGCCCGCAGGGAGCGGGCCCTCAGGCTCTCCGGCAAGCAT	324
QY	163	CATCGCCAGGGCCCGCAGGCGCTCCTGTGGAGCGCAGTCAACAGCAGAGCAGCAACAGC	222
Db	325	CATCGCCAGGGCCCGCAGGCGCTCCTGTGGAGCGCAGTCAACAGCAGAGCAGCAACAGC	384
QY	223	AGCAGCCATCATGAGAGGCGCTGGGGCTGTGGAGATCCCGAGTCCGCAACAGTCTTAACTCC	282
Db	385	AGCAGCCATCATGAGAGGCGCTGGGGCTGTGGAGATCCCGAGTCCGCAACAGTCTTAACTCC	444
QY	283	GGGGGAGCGAGAGCAGAGAGAGATGGGGGAGAGAGCCAGGCCCTTTCCGGGCGCGCTCG	342
Db	445	GGGGGAGCGAGAGCAGAGAGAGATGGGGGAGAGAGCCAGGCCCTTTCCGGGCGCGCTCG	504
QY	343	CGCTCGGCGCCCGCCCAACCTTGTGGCAGACACAGCGCATATGGCCGGAGCTCCGAGATG	402
Db	505	CGCTCGGCGCCCGCCCAACCTTGTGGCAGACACAGCGCATATGGCCGGAGCTCCGAGATG	564
QY	403	AGTACCGAGTTTGTGGACTCTCTTTAAGAGGAACTTCTCCGCCGAAGCGCGGGGCGCA	462
Db	565	AGTACCGAGTTTGTGGACTCTCTTTAAGAGGAACTTCTCCGCCGAAGCGCGGGGCGCA	624
QY	463	GCAACGCGAGATGCGGCAAGCTCCAGCTGAGCGCGAGTCTTCCAGTCCCTGGTGGGATCG	522
Db	625	GCAACGCGAGATGCGGCAAGCTCCAGCTGAGCGCGAGTCTTCCAGTCCCTGGTGGGATCG	684
QY	523	AACTTGGGCAAGGAGAGCTCCGCCCTTCCAGTACGCTTCCGTCACATCCCGAAA-TC	581
Db	685	AACTTGGGCAAGGAGAGAGCTCCGCCCTTCCAGTACGCTTCCGTCACATCCCGAAACTC	744
QY	582	CACCGGTTCCCATTTGCCCTGGGCAACCATTTGAATATGGAGGAAAGTAAGTTCCCTCAG	641
Db	745	CACCGGTTCCCATTTGCCCTGGGCAACCATTTGAATATGGAGGAAAGT-ACCTTCCCTCAG	803
QY	642	GCGTATGCAAAAAGAGAGATCCGCTGTGTAATCCTTTGAGAGGAGGTTGACCCAGATTCC	701
Db	804	GCGTATGCAAAAAGAGAGATCCGCTGTGTAATCCTTTGAGAGGAGGCTGACCCAGATTCC	863
QY	702	TTCCGGTGTGTGTGAAGCCACGGAAGG-TTGGTCCCATGCGAAGTTTGGGTTTCCCGC	760
Db	864	TTCCGGTGTGTGTGAAGCCACGGAAGGCTTGGTCCCATGGAAGTTTGGGTTTCCCGC	923
QY	761	CACAGCCCGCGGAAGTGGCTCCGTGGCCCCCGCCCTCAGGTTCCGGGGTTTCCCGCAGG	820
Db	924	CACAGCCCGCGGAAGTGGCTCCGTGGCCCCCGCCCTCAGGCTTCCCGCAGGCG	983
QY	821	CCTGGCTTAAGTACGAGCGCAGAGTTTAAACGTTTGTGTCAACCGGAGCCCGAGCCCGCGA	880
Db	984	CCTGGCTTAAGTACGAGCGCAGAGTTTAAACGTTTGTGTCAACCGGAGCCCGAGCCCGCGA	1043
QY	881	TGCGCTGGGGGCGCGTATCATGTAACCAATGTTAATAAAGCCCGCGTGTGTGCCAAAAAA	940
Db	1044	TGCGCTGGGGGCGCGTATCATGTAACCAATGTTAATAAAGCCCGCGTGTGTGCCAAAAAA	1103
QY	941	AA 942	
Db	1104	AA 1105	
RESULT 4			
AAH78430			
ID	AAH78430 standard, cDNA, 1105 BP.		
XX	AAH78430,		
AC			
XX			
DT	26-NOV-2001 (first entry)		
XX			
DE	Nucleotide sequence of protein associated with cell proliferation-1.		
XX			
KN	Human; cell proliferation; APOB-1; APOB-2; APOB-3; apoptosis; cancer;		

Query Match	Best Local Similarity	Matches	88.8%	Score	840.4	DB	22	Length	1105
Query	43	GGCCAGACGATGTTCCAGATCCGAGAGTTTGAGCCGAGTGCAGGAAAGATCCAGCTCT	102						
Db	205	GCCCCAGACATGTTCCAGATCCGAGAGTTTGAGCCGAGTGCAGGAAAGATCCAGCTCT	264						
Query	103	GCAGAGAGGGGCTGGGGCCGAGCCGCGAGGGGAGCGGGCCCTGAGCTCCGGCAAGCAT	162						
Db	265	GCAGAGAGGGGCTGGGGCCGAGCCGCGAGGGGAGCGGGCCCTGAGCTCCGGCAAGCAT	324						
Query	163	CATGCCAGGCCCCCAGAGGCTCTCTGTGGAGCCGACGTCAACGAGAGAGCAGCCAAACGAGC	222						
Db	325	CATGCCAGGCCCCCAGAGGCTCTCTGTGGAGCCGACGTCAACGAGAGAGCAGCCAAACGAGC	384						
Query	223	AGCAGCCATCATGAGAGGCGCTGGGGCTGTGAGATCCGAGATCCGACAGCTCTTACCC	282						
Db	385	AGCAGCCATCATGAGAGGCGCTGGGGCTGTGAGATCCGAGATCCGACAGCTCTTACCC	444						
Query	283	GGGGGAGAGGAG	342						
Db	445	GGGGGAGAGGAG	504						
Query	343	CGCTGGGAGCCCCCAACCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	402						
Db	505	CGCTGGGAGCCCCCAACCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	564						


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Db      58 GCCCAGAGCATGTTCCAGATCCAGAGTTTGAAGCCAGTGAAGCAAGAAAGCTCCAGCTCT 117
Qy      103 GCAGAGAGGGGCTTGGGCCCCAGGCCCGCAGAGGAGCGGGCCCTGAGGCTCCGGCAAGCAT 162
Db      118 GCAAGAGAGGGGCTTGGGCCCCAGGCCCGCAGAGGAGCGGGCCCTGAGGCTCCGGCAAGCAT 177
Qy      163 CATGCGCAGGCGCCCAAGGCTCTCTGTGGAGCGCCAGTCAACAGCAGAGAGCAGCAACGAC 222
Db      178 CATGCGCAGGCGCCCAAGGCTCTCTGTGGAGCGCCAGTCAACAGCAGAGAGCAGCAACGAC 237
Qy      223 AGCAGCATCATGAGAGG-CGCTGGGGGCTGTGAGATCCGGAGTGGCCACAGCTCCTACCC 281
Db      238 AGCAGCATCATGAGAGGCGCTGTGGAGTGTGAGATCCGGAGTGGCCACAGCTCCTACCC 297
Qy      282 CGCGGGAGCGAGAGAGCAGAGAGGAGTGGGGAGAGAGCCAGCCCTTTCGGGGCGGCTC 341
Db      298 CGCGGGAGCGAGAGAGCAGAGAGGAGTGGGGAGAGAGCCAG-CCTTTTCGGGGCGGCTC 356
Qy      342 CGCGTGGGCGCCCGCAACTCTGTGGAGCAGCAGCGCTATGGCGCGAGCTCCGAGAGAT 401
Db      357 CGCGTGGGCGCCCGCAACTCTGTGGAGCAGCAGCGCTATGGCGCGAGCTCCGAGAGAT 416
Qy      402 GAGTGAAGAGTTTGTGAGCTCTTTAAGAGAGGATCTTCTGCGCCGAGAGAGCGGGGAC 461
Db      417 GAGTGAAGAGTTTGTGAGCTCTTTAAGAGAGGATCTTCTGCGCCGAGAGAGCGGGGAC 476
Qy      462 AGCAAGCAGATGCGGCAAGAGCTCCAGCTGAGCAGCGAGCTTCCAGTCTGTGGAGATCG 521
Db      477 AGCAAGCAGATGCGGCAAGAGCTCCAGCTGAGCAGCGAGCTTCCAGTCTGTGGAGATCG 536
Qy      522 GAACTTGGGAGAGGAGAGCTCCGCGCTCCAGTGAAGCTTCCAGTCTGTGCAATCCGAA-T 580
Db      537 GAACTTGGGAGAGGAGAGCTCCGCGCTCCAGTGAAGCTTCCAGTCTGTGCAATCCGAAACT 596
Qy      581 CCACCCGTTCCCATTTGCCCTGGGAGCGATTTGAATTTGGAGAGAAATAGTCCCTCA 640
Db      597 CCACCCGTTCCCATTTGCCCTGGGAGCGATTTGAATTTGGAGAGAAAT-ACCTTCTCA 655
Qy      641 GGCCTATGCAAAAAGAGATCCGTGCTGTATCTTTGGAGGAGGATGACCGAGATTCC 700
Db      656 GGCCTATGCAAAAAGAGATCCGTGCTGTATCTTTGGAGGAGGATGACCGAGATTCC 715
Qy      701 CTTCCGCTGTGTGAGAGCAGAGAGG-TTGCTCCATCGGAAGTTTGGGTTTCCGC 759
Db      716 CTTCCGCTGTGTGAGAGCAGAGAGGCTTGCTCCATCGGAAGTTTGGGTTTCCGC 775
Qy      760 CCACAGCGCGGAGAGTGGCTCCGTGGCGCCGCTCAGGTTCCGGGGTTTCCCGAGGC 819
Db      776 CCACAGCGCGGAGAGTGGCTCCGTGGCGCCGCTCAGGCTCCGGGCTTTTCCCGAGGC 835
Qy      820 GCTTCGCTAAGTACGAGAGCAGATTTAACGTTGTACCGGAGACCCGAGCCCGCG 879
Db      836 GCTTCGCTAAGTACGAGAGCAGATTTAACGTTGTGTACCGGAGACCCGAGCCCGCG 895
Qy      880 ATGCGCTGGGGG-CGCTGATCAGTACCAATGTATATAAGCCGCGTGTGTC 933
Db      896 ATGCGCTGGGGGCGCTGCTCACTACCAATGTATATAAGCCGCGTGTGTC 950

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RESULT 6
AAT91561
ID AAT91561 standard; DNA; 944 BP.
XX AC AAT91561;
XX AT91561;

XX 15-JAN-1998 (first entry)
XX DE BBC6 gene for regulating cell death.
XX BB6 gene; cell death; cell cycle; Bcl2; human; ss.
XX Homo sapiens.
XX OS

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FH      Key      Location/Qualifiers
FT      CDS      67..567
FT      FT      /*tag= a
FT      FT      /product= BBC6
PN      US663316-A.
PD      02-SEP-1997.
PP      18-JUN-1996; ✓ 96US-0665617.
PR      18-JUN-1996; 96US-0665617.
PA      (CLON-) CLONTECH LAB INC.
PI      Xudong Y;
PI      WPI: 1997-447980/41.
DR      P-PSDB; AAM32476.
PT      Isolated BBC6 gene - encodes a protein that regulates cell death
PT      through interaction with Bcl-2
PS      Claim 2; Column 9-12; 7pp; English.
XX      CC      The present sequence represents an isolated nucleic acid which encodes
XX      CC      a protein of 166 amino acids. The sequence is disclosed as being a
XX      CC      gene called BBC6 which encodes a protein that regulates cell death
XX      CC      through interaction with Bcl-2. The DNA may be used for the production
XX      CC      of the recombinant protein, which can be used in unspecified therapeutic
XX      CC      or diagnostic procedures, as a molecular weight marker, and to raise
XX      CC      antibodies that can be used in unspecified diagnostic or therapeutic
XX      CC      applications and to reduce or eliminate the biological activity of the
XX      CC      BBC6 protein in vivo.
XX      SQ      Sequence 944 BP; 172 A; 313 C; 299 G; 160 T; 0 other;

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Query Match 77.9%; Score 737; DB 18; Length 944;
Best Local Similarity 94.3%; Pred. No. 4,7e-174;
Matches 842; Conservative 0; Mismatches 40; Indels 11; Gaps 7;

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Qy      43 GCCCAGAGCATGTTCCAGATCCAGAGTTTGAAGCCAGTGAAGCAAGAAAGCTCCAGCTCT 102
Db      58 GCCCAGAGCATGTTCCAGATCCAGAGTTTGAAGCCAGTGAAGCAAGAAAGCTCCAGCTCT 117
Qy      103 GCAGAGAGGGGCTTGGGCCCCAGGCCCGCAGAGGAGCGGGCCCTGAGGCTCCGGCAAGCAT 162
Db      118 GCAAGAGAGGGGCTTGGGCCCCAGGCCCGCAGAGGAGCGGGCCCTGAGGCTCCGGCAAGCAT 173
Qy      163 CATGCGCAGGCGCCCAAGGCTCTCTGTGGAGCGCCAGTCAACAGCAGAGAGCAGCAACGAC 222
Db      174 CATGCGCAGGCGCCCAAGGCTCTCTGTGGAGCGCCAGTCAACAGCAGAGAGCAGCAACGAC 231
Qy      223 AGCAGCATCATGAGAGGCGCTGTGGAGTGTGAGATCCGGAGTGGCCACAGTCTCTACCCC 282
Db      232 AGCAGCATCATGAGAGGCGCTGTGGAGTGTGAGATCCGGAGTGGCCACAGTCTCTACCCC 291
Qy      283 CGCGGGAGCGAGAGAGCAGAGAGGAGTGGGGAGAGAGCCAGCCCTTTCGGGGCGGCTCG 342
Db      292 CGCGGGAGCGAGAGAGCAGAGAGGAGTGGGGAGAGAGCCAGCCCTTTCGGGGCGGCTCGC 351
Qy      343 CGCTCGGGCGCCCGCAACTCTGTGGAGCAGCAGCGCTATGGCGCGAGCTCCGAGAGATG 402
Db      352 GCTCGGGCGCCCGCAACTCTGTGGAGCAGCAGCGCTATGGCGCGAGCTCCGAGAGATG 411
Qy      403 AGTGAAGAGTTTGTGAGCTCTTTAAGAGAGGATTTCTCGCCGAGAGAGCGGGGACA 462
Db      412 AGTGAAGAGTTTGTGAGCTCTTTAAGAGAGGATTTCTCGCCGAGAGAGCGGGGACA 471
Qy      463 GCAAGCAGATGCGGCAAGAGCTCCAGCTGAGCAGGAGCTTCCAGTCTGTGGATCGG 522
Db      472 GCAAGCAGATGCGGCAAGAGCTCCAGCTGAGCAGGAGCTTTCAGTCTGTGGATCGG 531

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QY 523 AACTGGGAGGAGGAACTCCGCCCCCTCCCACTGATCCTTCGTCACATCCCGAAA-TC 581
 DB 532 AACTTGGGAGGAGGAACTCCGCCCCCTCCCACTGATCCTTCGTCACATCCCGAAA-TC 591
 QY 582 CACCCGTTCCCATTTGCGCCCTGGGAGAGCATTTTGAATATGGAGAGTAAATTTCTCTAG 641
 DB 592 CACCCGTTCCCATTTGCGCCCTGGGAGAGCATTTTGAATATGGAGAGTAAATTTCTCTAG 650
 QY 642 GCTTATGCAAAAAGAGATCCGTCGTATCTTTGAGAGAGGTTGACCCAGATTCC 701
 DB 651 GCTTATGCAAAAAGAGATCCGTCGTATCTTTGAGAGAGGTTGACCCAGATTCC 710
 QY 702 TTTCCGCTGTGTGAAGCCAGGAGG-TTGTCCTCATGGAATTTTGGTTTCCGCC 760
 DB 711 TTTCCGCTGTGTGAAGCCAGGAGG-TTGTCCTCATGGAATTTTGGTTTCCGCC 770
 QY 761 CACACCCCGGAGAGTGTCTCCCTGGCCCCCTCAAGTTTCCGAGGTTTCCCGAGGCG 820
 DB 771 CACACCCCGGAGAGTGTCTCCCTGGCCCCCTCAAG-TCGGGCTTTTCCCGAGGCG 829
 QY 821 CTTGGCTATGATGAGGAGGAGGATTTTAACTGTTGTGACCGGAGACCCGAGCCCGGCGA 880
 DB 830 CTTGGCTATGATGAGGAGGAGGATTTTAACTGTTGTGACCGGAGACCCGAGCCCGGCGA 888
 QY 881 TCCCTTGGGAGGAGGAGGATTTTAACTGTTGTGACCGGAGACCCGAGCCCGGCGA 913
 DB 889 TCCCTTGGGAGGAGGAGGATTTTAACTGTTGTGACCGGAGACCCGAGCCCGGCGA 941

RESULT 7

ID AB054707
 ID AB054707 standard; cDNA; 842 BP.

AC AB054707;

XX 22-AUG-2002 (first entry)

DE Human ovarian antigen HCE4K28 cDNA, SEQ ID NO:587.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KM inflammatory condition; immune disorder; blood disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disorder;
 KM gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive; gene; ss.

OS Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.

XX 07-JUN-2000; 2000US-209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Biree CE, Rosen CA;

XX WPI, 2002-147878/19.

XX P-PSDB; ABP41630.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -

XX Claim 1; SEQ ID NO 587; 2922bp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents cDNA encoding a human ovarian antigen of the
 CC invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 842 BP; 156 A; 275 C; 285 G; 121 T; 5 other;

Query Match 57.7%; Score 546; DB 24; Length 842;
 Best Local Similarity 97.1%; Pred. No. 1.9e-126;

Matches 572; Conservative 4; Mismatches 10; Indels 3; Gaps 2;

QY 43 GCCAGAGCATGTTCCAGATCCAGAGTTTAAAGCGAGTGAAGAGGAGTCCAGCTCT 102
 DB 253 GCCAGAGCATGTTCCAGATCCAGAGTTTAAAGCGAGTGAAGAGGAGTCCAGCTCT 312
 QY 103 GCAGAGAGGGGCTGGGCGCCAGCCCGCAGAGGAGCGGGCTCTAGCTCCGCAAGAT 162
 DB 313 GCAGAGAGGGGCTGGGCGCCAGCCCGCAGAGGAGCGGGCTCTAGCTCCGCAAGAT 372
 QY 163 CATGCCAGGCTCCAGGCTCTTGTGAGACCGCAGTCAACAGCAGAGCAGCCAAACGAC 222
 DB 373 CATGCCAGGCTCCAGGCTCTTGTGAGACCGCAGTCAACAGCAGAGCAGCCAAACGAC 432
 QY 223 AGCAGCCTATGAGAGGCGCTGGGCTGTGAGATCCGGAATCCGACAGCTCTTACCCC 282
 DB 433 AGCAGCCTATGAGAGGCGCTGGGCTGTGAGATCCGGAATCCGACAGCTCTTACCCC 492
 QY 283 GCGGGAGCGAGAGCAGAGAGGAGTGGAGGAGGAGCCAGCCCTTTGGGGCGCGCTCG 342
 DB 493 GCGGGAGCGAGAGCAGAGAGGAGTGGAGGAGGAGCCAGCCCTTTGGGGCGCGCTCG 552
 QY 343 CGCTGGGCGCCCTCCAACTCTGAGCAGACAGGCTTATGAGCGGAGCTCTCGAGAGATG 402
 DB 553 CGCTGGGCGCCCTCCAACTCTGAGCAGACAGGCTTATGAGCGGAGCTCTCGAGAGATG 612
 QY 403 AGTACAGATTTTGTGAGCTCTTTAAGAGGAGACTTCTGCGCCGAGAGAGCGCGGCA 462
 DB 613 AGTACAGATTTTGTGAGCTCTTTAAGAGGAGACTTCTGCGCCGAGAGAGCGCGGCA 672
 QY 463 GCAAGCAGATGCGGCAAGCTCCAGCTGAGAGGAGGAGCTTCCAGTCTGTGGAGATCGG 522
 DB 673 GCAAGCAGATGCGGCAAGCTCCAGCTGAGAGGAGGAGCTTCCAGTCTGTGGAGATCGG 732
 QY 523 AACTTGGGAGGAGGAG-TCGCGCCCTTCAGATGATCTTGTGATCCAGTCCGAAA-TC 581
 DB 733 AACTTGGGAGGAGGAG-TCGCGCCCTTCAGATGATCTTGTGATCCAGTCCGAAA-TC 790

QY 582 CACCGGTTCCATTGCGCTGGGAGAGCCATTTTGAATATGGAAGAGTA 630
DB 791 CACCGGTTCCATTGCGCTGGGAGAGCCATTTTGAATATGGAAGAGTA 839

RESULT 8

AC84599
ID AAC84599 standard; DNA; 507 BP.

AC84599;
XX AAC84599;

DT 02-APR-2001 (first entry)

XX Human Bad protein encoding DNA.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW Bad; Bcl-2; tumour; cytostatic; de.

XX Homo sapiens.

XX MO200075184-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15449.

XX 04-JUN-1999; 99US-0137494.

XX (UYIA) UNIV YALE.

XX Zhang H, Tsvelkov IM, Kondo T;

XX WPI; 2001-061703/07.

XX P-PSDB; AAB48287.

PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT involves altering levels of proteins such as S-phase kinase associated
PT proteins 1, 2 and cullin/CDC53 proteins -

XX Examples; Page 102-103; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a
XX cell, using proteins selected from S-phase kinase associated proteins 1
XX and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
XX cullin/CDC53 family of proteins). The method is useful for altering the
XX level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
XX polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
XX detecting tumours, and in monitoring tumor treatment in a mammal. Agents
XX that modulate interactions between SKP and target proteins are useful for
XX treating tumours.

XX Sequence 507 BP; 99 A; 165 C; 175 G; 68 T; 0 other;

XX Query Match 53.6%; Score 507; DB 22; Length 507;

XX Best Local Similarity 100.0%; Pred. No. 8.9e-117;

XX Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 ATGTTCCAGATCCAGAGTTTGAAGCCGAGTGAGCGAGAGAGTCCAGCTTGCAGAGAG 111

DB 1 ATGTTCCAGATCCAGAGTTTGAAGCCGAGTGAGCGAGAGAGTCCAGCTTGCAGAGAG 60

QY 112 GACCTGGGAGCCGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 171

DB 61 GACCTGGGAGCCGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120

QY 172 GCCCGAGGCTCTCTGTGGAGCCAGTACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 231

DB 121 GCCCGAGGCTCTCTGTGGAGCCAGTACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 180

QY 232 CATGAGAGCGCTGGGAGTGTGGAGATCCGAGTCCGAGTCTTACCCGCGGAGAG 291

DB 181 CATGAGAGCGCTGGGAGTGTGGAGATCCGAGTCCGAGTCTTACCCGCGGAGAG 240
QY 292 GAGGACGACGAGAGGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 351
DB 241 GAGGACGACGAGAGGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 352 CCCCCCAACTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
DB 301 CCCCCCAACTCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 412 TTGTGAGATCTCTTAAG 471
DB 361 TTGTGAGATCTCTTAAG 420
QY 472 ATGGGAGAGAGCTTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 531
DB 421 ATGGGAGAGAGCTTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 532 AGGGAGAGAGCTTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558
DB 481 AGGGAGAGAGCTTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507

RESULT 9

AB281201
ID AB281201 standard; cDNA; 1454 BP.

AB281201;
XX AB281201;

DT 10-MAY-2003 (first entry)

XX Murine BAD encoding cDNA SEQ ID NO:3.

XX Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
XX virucide; infection; gene; ss.

XX Mus musculus.

XX WO2003012049-A2.

XX 13-FEB-2003.

XX 31-JUL-2002; 2002WO-US24177.

XX 31-JUL-2001; 2001US-308929P.

XX (UYCH-) UNIV CHICAGO.

XX Munger J, Roizman B;

XX WPI; 2003-248168/24.

XX P-PSDB; ABR39082.

PT Inducing apoptosis in a cell infected with herpes simplex virus, HSV,
PT by administering to the cell, a composition comprising an agent that
PT inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3 -

XX Disclosure; Page 167-168; 192pp; English.

XX The present invention describes a method (M1) for inducing apoptosis in
XX a cell infected with herpes simplex virus (HSV), which comprises
XX administering to the cell, a composition having an agent that inhibits
XX phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also
XX described is a method (M2) for treating a patient infected with HSV, by
XX administering to the patient, a composition comprising a peptide
XX comprising a sequence of 4-100 continuous amino acids of a 168 residue
XX amino acid sequence (see ABR39081), where the peptide comprises ser112,
XX ser135, or ser155, or their combinations. BAD has virucide activity.
XX M1 is useful for inducing apoptosis in a cell infected with HSV, where
XX the cell is in a human. M2 is useful for treating a patient infected
XX with HSV. The present sequence encodes murine BAD, which is given in the
XX exemplification of the present invention.

inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

Sequence 615 BP; 137 A; 181 C; 205 G; 92 T; 0 other;

Query Match	34.2%	Score 324; DB 19;	Length 615;
Best Local Similarity	80.0%	Pred No. 3.8e-71;	
Matches 413; Conservative	0; Mismatches 85;	Indels 18;	Gaps 2

QY 43 GCCCAGAGCATTTTCAGATCCCAAGGTTTGAAGCCAGATGAGGAGGAAAGCTCCACACTC 10.2
 Db 118 GCCCAGAGTAATTTCCAGATCCCAAGGTTTGAAGCCAGATGAGGAGGAAAGCGTAAGCT 17.7
 QY 103 GCAGAGAGGGGCGCTGGGGCCCCAGCCCCGACGGGGAAGGAGCCCTCCAGGCTCCGGCAAGCAT 16.2
 Db 178 ACAGATAGGGGCGCTGGGGCCCTTAGCTCTACTAGAGACCAAGC-----AGGT 22.2
 QY 163 CATCGCCAGGGCCCCAGGGCTCTCTGTGGGACGCGCACTACACAGCAGGAGACGCCAACACAGC 22.2
 Db 223 CCTTACTGTGGCCCCAGAGGTCTCTGTGGGAGACAATTCATCAGCAGGAGCGGGACGACCC 28.2
 QY 223 AGCAGCCATCATGAGAGGGCGCTGGGGCTGTGGAATCCGAGTGCACACAGCTCTTAACCC 28.2
 Db 283 AACCACTCAATCAGAGAGGCGCAGAGGGCTATAGGAACTCGAGTGCACAGTGGTATCCCA 34.2
 QY 283 GCGGGGACGAGGAGACACAGCAAGAGGATGGGGGAGAGACCAGCCCTTTGGGGCCCTCG 34.2
 Db 343 GCGGGGACCGAGAGAGATGAAGGATGAGAGAGAGACTTAAGCCCTTTTCAGAGACGCTCG 40.2
 QY 343 CGCTGGCGCGCCCCCAACTCTTGGGACGACACAGCGCTATGGCCGCGAGCTCCGAGAGATG 40.2
 Db 403 CGTGGGGCTCCCCCAATCTCTGGGACGAGCAGCGCTACGCGCGTGAAGCTCCAAAGATG 46.2
 QY 403 AGTGAAGATTTGTGAGCTCCTTTAAGAGGGGACTCTCGCCCGAAGAGCGGGGACAC 46.2
 Db 463 AGCGATGAATTTGAGGGTCTCTT---CAAGGGACTTCTCTGCCCCAAGAGCGCAGGCACCT 51.9
 QY 463 GCNAGCGCAGATGCGGCAAAAGCTTCACAGCTGGACGCGAGTCTTCCAGTCTTGATGGGATCGG 52.2
 Db 520 GCACAACAGATGGAACAAGCGCGCGGTGGACGCGCATTTATTCAGTCTCTGTGGATCGA 57.9
 QY 523 AACTTGGGACAGGGGAAGCTTCGCCCCCTCTCCCAATGA 55.8
 Db 580 AACTTGGGCAAAAGAGGCTCAACCCCTCTCCCAATGA 61.5

RESULT 14
AAV27836
ID AAV27836 standard; cDNA; 615 BP

AC AAV27836;

DT 07-OCT-1998 (first entry)

DE Mutant BCL-XL/BCL-2 associated cell death regulator encoding cDNA #3.

KM Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein.
KM serine substituted mutant; apoptosis; cancer; viral infection; ss.

OS	Mus sp.
OS	Synthetic.

XX	Location/Qualifiers
PH	1..615
FT	/*tag= a
FT	/product= "mutant BAD protein
FT	

PN WO9817682-A1

PD 30-APR-1998

PF 17-OCT-1997; 97WO-US19175.

PR 18-OCT-1996; 96US-0733505.

PA (UNIW) UNIV WASHINGTON
...

PI KORMEYER SU

DR WPI; 1998-261422/23

XX

PT useful for, e.g. treating reduced apoptosis such as in cancer or

PS Claim 16; Page 63; 95pp; English.

The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulatory) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence encodes a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD. By usual immunoassays, Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

Sequence 615 BP; 137 A; 181 C; 205 G; 92 T; 0 other;

Query Match	34.2%	Score 324	DB 19	Length 615
Best Local Similarity	80.0%	Pred. No.	3.8e-71	
Matches 413; Conservative	0	Mismatches	85	Indels 18; Gaps 2

QY	43	GGCCAGAGCATTTCCAGATCCCAAGTTTGGCCGAGGACAGAGAACTCCACTCT	102
Db	118	GCCCAAGATATTTCCAGATCCCAAGTTTGAAGCCGAGGACAGAAAGCTAGTGCT	177
QY	103	GCAGAGAGGGGCTGTGGGCCCAAGCCCGCAGGGGAGAGGGCCCTCAGGCTTCGGCAAGCAT	162
Db	178	ACAGATAGGGGCGTGTGGGCCCTAGGCTCACTGAGGACAGAC-----AGGT	222
QY	163	CATGCCCAGGCCCCAGGCTCTGTGGGACGCGCAGTACACAGAGGAGCAACCAACGAGC	222
Db	223	CCCTACTGGCCCCAGGATCTCTGGGGAGCAACATTCATCACAGAGGAGCGGCGACGACAC	282
QY	223	AGCACCATCATGAGGAGCGCTGTGGGCTGTGAGATTCGGAGATCGCCACAGCTCTTACCCC	282
Db	283	AACAGTCACTCATGAGAGGCGCAGAGGGGCTATGAGAGACTGGAGTGCACAGTGTGTAACCA	342

QY 283 GCGGGAGCGAGCAGCAGAGGAGATGGGGAGAGCCCGCTTTCGGGGCGGCTCG 342
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 QY 343 GCGTGGGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 402
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 DB 463 AGCGATGATTTGAGGCTTCTT---CAAGGAGCTTCTGCGCGGAGAGCGGCGACT 519
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 DB 520 GCAACACAGATGGCAGAGAGCGCGGCTGAGCGGATTAATCAATCTGTTGGATCGA 579
 QY 523 AACTTGGGCGAGGAGGAGCTTCCGCGGCTTCCCACTGA 558
 DB 580 AACTTGGGCGAGAGGAGGCTTCCAGCCCTCCCACTGA 615

RESULT 15

AA000248
 ID AA000248 standard; DNA; 1704 BP.

AC AA000248;

DT 31-MAY-2001 (first entry)

DE Bad-DTRR apoptosis-modifying fusion protein, DNA sequence.

KW Mouse; Bad-DTRR; apoptosis; cancer; spinal muscular atrophy; ds;
 KW diphtheria toxin receptor binding domain; DTRR; neoplasm; tumour;
 KW hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;
 KW transient ischaemic neuronal injury; stroke; spinal cord injury;
 KW Huntington's disease; diphtheria toxin translocation domain.
 OS Chimeric - Mus sp.
 OS Chimeric - Corynebacterium diphtheriae.
 OS Chimeric - Synthetic.

FT Key Location/Qualifiers
 FT CDS 1..1704
 FT /tag= a
 FT /product= "Bad-DTRR fusion protein"
 FT /note= "DTRR is diphtheria toxin translocation domain"
 FT misc_feature 7..36
 FT /tag= b
 FT /note= "10x histidine tag"

W0200112661-A2.

PD 22-FEB-2001.

PF 15-AUG-2000; 2000WO-US22293.

PR 16-AUG-1999; 99US-0149220.

PA (HARD) HARVARD COLLEGE.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Youle RJ, Liu X, Collier RJ;

DR MPI: 2001-218343/22.

DR P-PSDB; AAU00220.

PT Novel fusion protein for modifying apoptosis in target cell and
 PT reducing apoptosis after transient ischaemic neuronal injury, has two
 PT domains which target protein to a cell and modifies apoptotic response
 PT of cell -

PS Claim 5; Page 57-59; 65pp; English.

CC The sequence represents the coding sequence of Bad-DTRR apoptosis-
 CC modifying fusion protein comprising Bad gene sequence fused via a short
 CC linker to diphtheria toxin translocation domain (DTRR). The
 CC functional apoptosis-modifying fusion protein is capable of binding a
 CC target cell and integrating into or crossing a cellular membrane of the
 CC target cell. The apoptosis-modifying fusion protein comprises at least
 CC two domains: the DTR domain, which targets the fusion protein to the
 CC target cell and the Bcl-XL domain, which modifies an apoptotic response
 CC of the target cell. The fusion protein is useful for modifying
 CC (inhibiting or enhancing) apoptosis in a target cell, such as neuron,
 CC lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or
 CC hyper-proliferative cell or an adipocyte. It is also useful for reducing
 CC apoptosis in a subject after transient ischaemic neuronal injury.
 CC especially spinal cord injury. The fusion protein may be used to treat
 CC various diseases and injury conditions through inhibition or enhancement
 CC of apoptotic cellular response, including neurodegenerative disorders
 CC such as Alzheimer's disease, Huntington's disease, spinal muscular
 CC atrophy, stroke episodes and unregulated cell growth as in tumours and
 CC various cancers. The apoptosis-modifying fusion protein can be delivered
 CC effectively throughout the body and targeted to selective tissue and
 CC cells.

SQ Sequence 1704 BP; 470 A; 395 C; 444 G; 395 T; 0 other;

Query Match 34.1%; Score 322.4; DB 22; Length 1704;
 Best Local Similarity 79.8%; Pred. No. 1.2e-70;
 Matches 412; Conservative 0; Mismatches 86; Indels 18; Gaps 2;

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 DB 181 GCCCAGAGATGTCAGATCCAGATTTGAGCGGAGTACAGAGAGATCCAGCTCT 240
 QY 103 GAGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 162
 DB 241 AAGAGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 285
 QY 163 CATGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 222
 DB 286 CCTACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 345
 QY 223 AGCAGCATATGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 282
 DB 346 AACAGTATATGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 405
 QY 283 GCGGAG 342
 DB 406 GCGGAG 465
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 DB 466 CGTGGCGGCTCCCGCAATCTCTGGGAGCGAGCGGCTTACGCGCTTGGAGT 525
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 DB 526 AGCGATGATTTGAGGCTTCTT---CAAGGAGCTTCTGCGCGGAGAGCGGAG 582
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 DB 643 AACTTGGGCGAGAGGAGGCTTCCAGCCCTCCCACTGA 678

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GenCore version 5.1.6
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	737	77.9	944	1	US-08-665-617-1
6	344	36.4	1472	1	US-08-333-565-1
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24	39	4.1	882	4	US-09-252-991A-10163
25	38.6	4.1	435	4	US-09-397-787-162
26	38.4	4.1	4403765	3	US-09-103-840A-2
27	38.4	4.1	4411529	3	US-09-103-840A-1

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C 29	38.2	4.0	1239	4	US-09-252-991A-9713	Sequence 9713, Ap
C 30	38.2	4.0	1719	4	US-09-252-991A-9632	Sequence 9632, Ap
C 31	38.2	4.0	3654	4	US-09-252-991A-9533	Sequence 9533, Ap
C 32	37.6	4.0	1476	4	US-09-434-288-12	Sequence 12, Appl
C 33	37.6	4.0	3147	2	US-08-781-802-7	Sequence 7, Appl
C 34	37.6	4.0	3147	3	US-08-694-078-7	Sequence 7, Appl
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C 36	37.2	3.9	1608	4	US-09-252-991A-8274	Sequence 8274, Ap
C 37	37.2	3.9	2055	4	US-09-252-991A-8047	Sequence 8047, Ap
C 38	37.2	3.9	2298	4	US-09-252-991A-8220	Sequence 8220, Ap
C 39	37	3.9	1329	4	US-09-252-991A-9571	Sequence 9571, Ap
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C 41	36.6	3.9	738	4	US-09-252-991A-13548	Sequence 13548, A
C 42	36.6	3.9	1053	4	US-09-252-991A-13694	Sequence 13694, A
C 43	36.6	3.9	1164	4	US-09-252-991A-13896	Sequence 13896, A
C 44	36.6	3.9	1293	4	US-09-252-991A-13447	Sequence 13447, A
C 45	36.4	3.8	5045	3	US-09-390-721-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-717-123-1
; Sequence 1, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilmann
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 946 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..555
; US-08-717-123-1
Query Match 100.0%; Score 946; DB 2; Length 946;
Best Local Similarity 100.0%; Pred. No. 9e-232;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 gggcctagggcgccggtcgaagatcgagcttgaggccagagcatgttcag 60
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RESULT 2

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US-09-375-257-1
; Sequence 1, Application US/09375257
; Patent No. 6504022
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Olerendorf, Tilmann
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D1

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; CURRENT APPLICATION NUMBER: US/09/375,257
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-375-257-1

Query Match      100.0%; Score 946; DB 4; Length 946;
Best Local Similarity 100.0%; Pred. No. 9e-232;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGCTTAGGGGCGCGGGCTCAGGGGCTTCAGATCGGGCTTGGGCCAGAGCATGTTCCAG 60
Db      1 GGGGCTTAGGGGCGCGGGCTCAGGGGCTTCAGATCGGGCTTGGGCCAGAGCATGTTCCAG 60
Qy      61 ATCCAGAGTTTGAAGCCGAGTGAAGCAGAGAAAGACTCAAGTCTGCGAGAGAGGGGCTTGAGG 120
Db      61 ATCCAGAGTTTGAAGCCGAGTGAAGCAGAGAAAGACTCAAGTCTGCGAGAGAGGGGCTTGAGG 120
Qy      121 CCCAGCCCCGACGGGGGACGGGGCTTCAGAGCTCCGGCAAGCATCTCCAGGCCCAAGGC 180
Db      121 CCCAGCCCCGACGGGGGACGGGGCTTCAGAGCTCCGGCAAGCATCTCCAGGCCCAAGGC 180
Qy      181 CTCTGTGGAGACCGCACTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db      181 CTCTGTGGAGACCGCACTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy      241 GCTGGGAGCTGTGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAG 300
Db      241 GCTGGGAGCTGTGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAGATCCGAG 300
Qy      301 GAAGGAGATGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db      301 GAAGGAGATGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy      361 CTCTGGGAGAGACCGCTATAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db      361 CTCTGGGAGAGACCGCTATAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy      421 TCCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db      421 TCCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      481 AGCTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db      481 AGCTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy      541 TCCGCCCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db      541 TCCGCCCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy      601 GGGGAGCATTATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 660
Db      601 GGGGAGCATTATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 660
Qy      661 CCGTCTGTATCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db      661 CCGTCTGTATCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy      721 ACAGAGAGTGTGTCCATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db      721 ACAGAGAGTGTGTCCATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy      781 CCGTGGGCCCCGCTCAGAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db      781 CCGTGGGCCCCGCTCAGAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy      841 AGGTTTAACCGTTGTGTGTCACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db      841 AGGTTTAACCGTTGTGTGTCACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

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QY 901 GTCACAAATGTTAATAAGCCCGTGTGTGCCCAAAAAAAAAA 946
DB 901 GTCACAAATGTTAATAAGCCCGTGTGTGCCCAAAAAAAAAA 946

RESULT 3

US-08-985-335-2
; Sequence 2, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; TELEPHONE: 650-845-4166
; TELEFAX: 650-845-0555
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: 358673
; CLONE: SYNORAB01
; US-08-985-335-2

Query Match 88.8%; Score 840.4; DB 3; Length 1105;
Best Local Similarity 97.9%; Pred. No. 7e-205;
Matches 883; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

QY 43 GCCCAGAGCATGTCAGATCCAGAGTTGAGCCGAGTACAGAGAGTCCAGCTT 102
DB 205 GCCCAGAGCATGTCAGATCCAGAGTTGAGCCGAGTACAGAGAGTCCAGCTT 264
QY 103 GCGAGAGAGGCTGTGGGCCCCCGAGGAGAGGAGGCTTCCGCGAAGCAT 162
DB 265 GCGAGAGAGGCTGTGGGCCCCCGAGGAGAGGAGGCTTCCGCGAAGCAT 324
QY 163 CATCCGACAGGCCCCGAGGCTTCTGTGGAGGCGCAGTACACAGAGAGGCAACCGC 222
DB 325 CATCCGACAGGCCCCGAGGCTTCTGTGGAGGCGCAGTACACAGAGAGGCAACCGC 384
QY 223 AGCAGCATCATGAGGCGCTGGGGCTGTGAGATCCGAGTCCGACAGCTCTAACC 282

DB 385 AGCAGCATCATGAGGCGCTGGGGCTGTGAGATCCGAGTCCGACAGCTCTAACC 444
QY 283 GCGGAGAGGAGAGAGAGAGAGTGGGAGAGAGCCAGCCCTTTTGAGGCGGCTG 342
DB 445 GCGGAGAGGAGAGAGAGAGTGGGAGAGAGCCAGCCCTTTTGAGGCGGCTG 504
QY 343 CGCTCGGCGCCCCCAACTCTGTGGCAGACAGCGCTATGAGCCGAGCTCCGAGATG 402
DB 505 CGCTCGGCGCCCCCAACTCTGTGGCAGACAGCGCTATGAGCCGAGCTCCGAGATG 564
QY 403 AGTGAAGATTGTGAGCTCTTTAAGAGGAGCTTCTCGCCGAGAGAGCGGAGCA 462
DB 565 AGTGAAGATTGTGAGCTCTTTAAGAGGAGCTTCTCGCCGAGAGAGCGGAGCA 624
QY 463 GGAAGGAGATGCGGCAAGCTCCAGCTGAGAGGAGCTTCACTCGTGGGAGATCG 522
DB 625 GGAAGGAGATGCGGCAAGCTCCAGCTGAGAGGAGCTTCACTCGTGGGAGATCG 684
QY 523 AACTGGGACAGGAGAGCTCCGCCCCCTCCAGTACCTTCCGATCCAGTCCGAAA-TC 581
DB 665 AACTGGGACAGGAGAGCTCCGCCCCCTCCAGTACCTTCCGATCCAGTCCGAAA-TC 744
QY 582 CACCCGTTCCATTCCTGCGGACGCAATTTGAATATGAGAGAGTAACTTCCCTAG 641
DB 745 CACCCGTTCCATTCCTGCGGACGCAATTTGAATATGAGAGAGTAACTTCCCTAG 803
QY 642 GCTATGAGAGAGAGAGTCCGCTGCTATCTTTGAGGAGAGGTTGACCAATCC 701
DB 804 GCTATGAGAGAGAGAGTCCGCTGCTATCTTTGAGGAGAGGTTGACCAATCC 863
QY 702 TTCCGCTGTGTGTAAGCAGAGAGG-TTGGTCCATGAGAGTTTGGTTTCCGCC 760
DB 864 TTCCGCTGTGTGTAAGCAGAGAGG-TTGGTCCATGAGAGTTTGGTTTCCGCC 923
QY 761 CACAGCCCGGAGAGTCTCGTGCCCGCCCTCAGGTTCCGAGGTTTCCCGAGCG 820
DB 924 CACAGCCCGGAGAGTCTCGTGCCCGCCCTCAGGTTCCGAGGTTTCCCGAGCG 983
QY 821 CCGTGGCTAATGAGAGAGGTTTAACTGTTGTACACCGGAGCCGAGGCCCCGGA 880
DB 984 CCGTGGCTAATGAGAGAGGTTTAACTGTTGTACACCGGAGCCGAGGCCCCGGA 1043
QY 881 TGCCCTGGGAGCGGATCAGTACCAATGTTAATAAGCCCGAGTGTGTGCAAAAAA 940
DB 1044 TGCCCTGGGAGCGGATCAGTACCAATGTTAATAAGCCCGAGTGTGTGCAAAAAA 1103
QY 941 AA 942
DB 1104 AA 1105

RESULT 4

US-09-410-372-2
; Sequence 2, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410.372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985.335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: 358673
CLONE: SYNORAB01
US-09-410-372-2

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Query Match 88.8%; Score 840.4; DB 3; Length 1105;

Best Local Similarity 97.9%; Pred. No. 76-205; Mismatches 16; Indels 3; Gaps 3;

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Matches 883; Conservative 0; Mismatches 16; Indels 3; Gaps 3;
43 GCCCAGACATGTTCCAGATCCAGAGTTTGGAGCCGAGTGAAGAGAGTCCAGCTCT 102
205 GCCCAGACATGTTCCAGATCCAGAGTTTGGAGCCGAGTGAAGAGAGTCCAGCTCT 264
103 GCAGAGAGGGGCTTGGGCCCCCAGCCCGCAGGGGAGCGG3CCTTCAAGGCTCCGGCAGCAT 162
265 GCAGAGAGGGGCTTGGGCCCCCAGCCCGCAGGGGAGCGG3CCTTCAAGGCTCCGGCAGCAT 324
163 CATGGCCAGGGCCCGGAGGCTCTGTTGGAGACCGCATCCAGCAGAGAGAGAGAGAGAGCAGC 222
325 CATGGCCAGGGCCCGGAGGCTCTGTTGGAGACCGCATCCAGCAGAGAGAGAGAGAGAGCAGC 384
223 AGCAGCCATCATGAGAGCGCTGGGGCTGTGAGATCCGAGTCCGACAGCTCTTACCC 282
385 AGCAGCCATCATGAGAGCGCTGGGGCTGTGAGATCCGAGTCCGACAGCTCTTACCC 444
283 GCGGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 342
445 GCGGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 504
343 GCGGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 402
505 GCGGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 564
403 AGTGAAGATTGTGAGATCTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
565 AGTGAAGATTGTGAGATCTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 624
463 GCAAGCAGATGCGGCAAGAGCTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
625 GCAAGCAGATGCGGCAAGAGCTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 684
523 AACTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 581
685 AACTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 744
582 CACCGGTTCCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
745 CACCGGTTCCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
642 GCTATGCAAAAAGAGATCCGTTGATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701

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Db 804 GCTATGCAAAAAGAGATCCGTTGATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 863
Qy 702 TTCGGTGTGTGTAAGCCAGAGAG-TTGATCCATCGAGATTGTGGGTTTCGCC 760
Db 864 TTCGGTGTGTGTAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923
Qy 761 CACAGCCGCGGAGAGTGTCTCGTGGCCCGCCCTCAGTTCCGGGGTTTCCCCAGAGCG 820
Db 924 CACAGCCGCGGAGAGTGTCTCGTGGCCCGCCCTCAGCTCCGGGCTTTCGCCAGAGCG 983
Qy 821 CTTCGGTGTGTGTAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 880
Db 984 CTTCGGTGTGTGTAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043
Qy 881 TGCCCTGGGGGCGGTGATGATCAATGTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 940
Db 1044 TGCCCTGGGGGCGGTGATGATCAATGTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
Qy 941 AA 942
Db 1104 AA 1105

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RESULT 5

US-08-665-617-1

Sequence 1, Application US/08665617

Patent No. 566316

GENERAL INFORMATION:

APPLICANT: Xudong, Yin

TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,617

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: CL-8

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 944 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-665-617-1

Query Match 77.9%; Score 737; DB 1; Length 944;

Best Local Similarity 94.3%; Pred. No. 1,4e-178; Indels 11; Gaps 7;

Matches 842; Conservative 0; Mismatches 40; Indels 11; Gaps 7;

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43 GCCCAGACATGTTCCAGATCCAGAGTTTGGAGCCGAGTGAAGAGAGAGTCCAGCTCT 102
58 GCCCAGACATGTTCCAGATCCAGAGTTTGGAGCCGAGTGAAGAGAGAGTCCAGCTCT 117
103 GCAGAGAGGGGCTTGGGCCCCCAGCCCGCAGGGGAGCGG3CCTTCAAGGCTCCGGCAGCAT 162

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Db      118 GCAGAGAGGGGCTGGCGC-----AGCCCGCAGGAGCGGGCCCTCAGAGCTCCGGCAAGCAT 173
Qy      163 CATCGCAGAGGCCCGCAGGCTCTGTGGAGCGCCAGTCACACAGCAGGAGGAGCAACACAG 222
Db      174 CATCGCAGAGGCCCGCAGG--TCCGTGGAGCGCCAGTCACACAGCAGGAGGAGCAACACAG 231
Qy      223 AGCAGCATCATGAGAGCGCTGGAGCTGTGAGATCCGAGATCCGACAGCTCTTACCCC 282
Db      232 AGCAGCATCATGAGAGCGCTGGAGCTGTGAGATCCGAGATCCGACAGCTCTTACCCC 291
Qy      283 GGGGGGACCGAGAGCAGCAGAGGATGGGGGAGAGGCCAGCCCTTTTGGGGCGCGCTCG 342
Db      292 GGGGGGACCGAGAGCAGCAGAGGATGGGGGAGAGGCCAGCCCTTTTGGGGCGCGCTCG 351
Qy      343 GCTCGGCGCGCCCGCAGGCTCTGGGAGAGCAGCGCTATGGCGGAGGCTCGGAGAGATG 402
Db      352 GCTCGGCGCGCCCGCAGGCTCTGGGAGAGCAGCGCTATGGCGGAGGCTCGGAGAGATG 411
Qy      403 AGTGAAGAGTTGTGAGCTCTTTAAGAGAGACTTCTCGCCGAGAGAGCGCGGAGCA 462
Db      412 AGTGAAGAGTTGTGAGCTCTTTAAGAGAGACTTCTCGCCGAGAGAGCGCGGAGCA 471
Qy      463 GCAAGCGAGATGCGGAGAGCTCAGCTGAGCGGAGCTTCCAGTCTCTGTGGAGATCG 522
Db      472 GCAAGCGAGATGCGGAGAGCTCAGCTGAGCGGAGCTTCCAGTCTCTGTGGAGATCG 531
Qy      523 AACTGGGAGGAGGAGCTCGCGCCCTCCAGTGACTTCCGTCCACATCCCGAA--TC 581
Db      532 AACTGGGAGGAGGAGCTCGCGCCCTCCAGTGACTTCCGTCCACATCCCGAAATC 591
Qy      582 CACCGGTTCCATTTGCTGGGAGCGCATTTTGAATGGAGAGAGTAAGTTCCCTCAG 641
Db      592 CACCGGTTCCATTTGCTGGGAGCGCATTTTGAATGGAGAGAGTAAGTTCCCTCAG 650
Qy      642 GCTTATGCAAAAGAGATCCGTCTGTATCTTTGAGAGAGAGGTTGACCAATGCC 701
Db      651 GCTTATGCAAAAGAGATCCGTCTGTATCTTTGAGAGAGAGGTTGACCAATGCC 710
Qy      702 TTCGGGTGTGTGAAGCCAGGAGG--TTGGTCCATGAGAAAGTTTGGTTTCCGCG 760
Db      711 TTCGGGTGTGTGAAGCCAGGAGGCTTGTGCTCCATGAGAAAGTTTGGTTTCCGCG 770
Qy      761 CACAGCCCGCGAGAGTGTCTCCGTGGCCCGGCTTCAGGTTCCGGGATTTCCCGAGG 820
Db      771 CACAGCCCGCGAGAGTGTCTCCGTGGCCCGGCTTCAGG--TCCGGGCTTTCCCGAGG 829
Qy      821 CCGTGGCTTATGAGCGAGCGAGTTTAACTGTTGTCTACCGGAGACCGGAGCCCGCG 880
Db      830 CCGTGG--TAACTGCGGAGCGAGGTTTAACTGTTGTCTACCGGAGACCGGAGCCCGCG 888
Qy      881 TGCCCTGGGGGCGGATGATGATCAAAATGTTAATTAAGCCCGCGTGTGCG 933
Db      889 TGCCCTGGGGGCGGATGATGATCAAAATGTTAATTAAGCCCGCGTGTGCG 941

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RESULT 6
US-08-333-565-1
; Sequence 1, Application US/08333565
; Patent No. 562852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-333-565-1

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Query Match      36.4%; Score 344; DB 1; Length 1472;
Best Local Similarity 76.9%; Pred. No. 1.6e-78;
Matches 480; Conservative 0; Mismatches 120; Indels 24; Gaps 4;

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Qy      43 GCCCAGACATGTTCCATATCCAGATGTTGAGCTGAGTGAAGAGAGAGCTCCAGCTCT 102
Db      588 GCCCAGATATGTTCCATATCCAGATGTTGAGCTGAGTGAAGAGAGAGCTTATGCTCT 647
Qy      103 GCAGAGAGGAGCTGGGCGCCAGCGCCGAGGAGAGCGGCGCTCAGCGCTCGGCAAGAT 162
Db      648 ACAATAGAGGAGCTGGGCGCCAGCGCTTACCTTCACTAGAGACAGCC-----AGCT 692
Qy      163 CATCGCAGGCGCCCGCAGGCTCTGTGGAGCGCCAGTCAACAGCAGAGCAGCAACAGC 222
Db      693 CCTTACCTGGGCGCCCGCAGGCTCTGTGGAGCGCAACATTTATCAGCAGGAGCGGAGCAGC 752
Qy      223 AGCAGCATCATGAGAGCGCTGGGCTGTGAGATCCGAGATCCGACAGCTCTTACCCC 282
Db      753 AACAGTATCATGAGAGCGGAGGCTATGAGAGCTCGAGTCCGACAGTTCGTAACCA 812
Qy      283 GCGGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 342
Db      813 GCGGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 872
Qy      343 CGCTCGGCGCCCGCAGACCTCTGAGCAGCAGAGGCTATGAGCGAGCTCCGAGAGATG 402
Db      873 CGTTGGCTCCCGCAGACCTCTGAGCAGCAGAGGCTATGAGCGAGCTCCGAGAGATG 932
Qy      403 AGTGAAGAGTTGTGAGCTCTTTAAGAGAGACTTCTCGCCCGAGAGAGCGGAGCA 462
Db      933 AGCGATGAGTTGAGAGGTTCTT---CAAGGAGACTTCTCCCGCAAAAGAGCGAGGCACT 989
Qy      463 GCAAGCGAGATGCGGCAAAAGCTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
Db      990 GCAACAGAGATGCGCAAAAGCGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1049
Qy      523 AACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 581
Db      1050 AACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1107
Qy      582 CACCGGTTCCATTTGCTGGGAGAGCAATTTTGAATATGAGAGAGAGTAAGTTCCCTCAG 641
Db      1108 ---CTTACCGGCTCCCGCGCGCGCAATATGAGGAGAGAGAGAGAGAGAGAGAGCT 1164
Qy      642 GCTTATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
Db      1165 TAGGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1188

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RESULT 7

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Oy 103 GGAGAGAGGGGCTGTGGGCCCCAGCCCCGCGAGGGGAGCGGGCCCTTCAGGCTCCGGCAAGCAT 162
 Db 178 ACGATAGAGGGGCTGGGGCCCTTAAGCTCCTACAGAGGACCAAGC-----AGGT 222
 Oy 163 CATGCGCAGAGCCCGAGGCTCTGTGTGGAGCGCCAGTCAACGAGAGAGACCAACCAAGC 222
 Db 223 CCTTACTGTGGCCCGAGGTTCTCTGGGGAGAGCAATTTCATAGCAGGGAGCGGGAGCGCAAC 282
 Oy 223 AGCAGGCATCATGGAGGGCGTGGGGGCTGTGGAGATCCGGAGTGGCCAAGCTCCTTACCCC 282
 Db 283 AACAGTCATCATGGAGGGCGAGGGGCTATGGAGACTGGAGTGGCCACAATTGTGTACCA 342
 Oy 283 GCGGGGACGAGAGACACACAAGGAGTGGGGGAGAGAGCCAGCCCTTTTCGGGGCCGCTCG 342
 Db 343 GCGGGGACCGAGAGAGATGAGAGGAGTGAAGAGAGATTAGCCCTTTTCGAGGACGCTCG 402
 Oy 343 CGCTGGGCGCCCCCCCCAACCTTGTGGGACGACACAGCGCTATGCGCCGCGAGCTCCGAGAGATG 402
 Db 403 CGTTGGGCTCCCCCAATCTGTGGGACGAGCGCTACCGCGTGTGACTCCAAAGGATG 462
 Oy 403 AGTGCAGAGTTGTGTGACTCTTTAAGAAAGGACCTTCTGCGCCGAGAGAGCGGGGACA 462
 Db 463 AGCGATGAGTTTGAGGGTTCCTT---CAAGGACCTTCTGCCCCAAAGAGCGCAGGCACT 519
 Oy 463 GCAACGCAAGATCGGCAAAAGCTTCAGCTGAGCGCGAGTCTTCCAGTCTTGTTGGAGATCGG 522
 Db 520 GCAAACACAGATCGCAAAAGCGCGGCTG6AGCGCATTAATTCAGTCTGTGGATCGA 579
 Oy 523 AACTTGGGAGGGGAAAGTCCGCGCCCTCCCAAGTGA 558
 Db 580 AACTTGGGCAAAAGAGGCTCAACCCCTCCCAAGTGA 615

RESULT 9
 US-08-661-479-3
 Sequence 3, Application US/08661479
 Patent No. 5834209
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
 TITLE OF INVENTION: REGULATOR
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/661,479
 FILING DATE: 11-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/333,565
 FILING DATE: 31-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000700
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 615 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

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?      TOPOLOGY: linear
?
?      MOLECULE TYPE: CDNA
?
?      FEATURE:
?          NAME/KEY: misc_feature
?      LOCATION: 1..615
?      OTHER INFORMATION:
?      OTHER INFORMATION:
?          /note="Polynucleotide coding
?          sequence of mouse BAD CDNA."
US-08-661-479-3

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Query Match	34.6%;	Score 327.2;	DB 2;	Length 615;
Best Local Similarity	80.4%;	Pred. No. 2.5e-74;		
Matches 415;	Conservative 0;	Mismatches 83;	Indels 18;	Gaps 2;

Qy	4	GCCCAAGATGTTCCAGATCCCAAGATTGAGCCGAGTGAAGAAATCCAGCTCT	102
Db	118	GCCCAAGATGTTCCAGATCCCAAGATTGAGCCGAGTGAAGAAAGCTGAGTCT	177
Qy	103	GCAGAGGGGGCTGGGCCCCAGCCCCCAGGGGACGGGCCCTCGGCAAGCAT	162
Db	178	ACAGATAGGGGGCTGGGCCCTTAGCTCACTAGAGCAAGCC-----AGGT	222
Qy	163	CATGCGCAGGGCCCAAGGCTCTCTGTGGAACGCAGTCAACAGCAGAGACCCAAACAGC	222
Db	223	CCCTAAGTGGCCCCAGGTCTCTCTGGGGAGCAACATTCATCAGCAGGACGGGACGACCC	282
Qy	223	AGAGAGCATCATGAGAGGCGCTGGGGCTGTGGAGATCCGGAATCCCAACAGTCTTACCCC	282
Db	283	AACAGTCATCATGAGAGGCGCAGGGGCTGTGAGACTGGGAATGCCACAGTTGCTTACCA	342
Qy	283	GCGGGGACGAGAGACGACGAGAGGATGGGGGAGAGCCAGCCCCCTTGGGGGCGCTCG	342
Db	343	GCGGGGACGAGAGAGATGAGAGGATGGAGAGAGAGCTTACCCCTTTTCAGAGACGCTCG	402
Qy	343	CGCTGGGCGCCCCCAACTCTTGGGACAGACAGGCTATGCGCGGAGCTCCGAGGATG	402
Db	403	CGTGGGCTCCCCCAACTCTCTGGGCAAGCGAGCTTACGCGGTGAGCTCCGAAGATG	462
Qy	403	AGTACGAGATTGTGGACTCTTTAAGAGGACCTTCTCGCCCCGAAGAGCGCGGACCA	462
Db	463	AGGAGTAGATTGAGGGTTCCTT---CAAGGGACCTTCTCGCCAAAGAGGCGAGCACT	519
Qy	463	GCACGCGAGATGCGGCAAGGCTTCAGCTGAGACGCGAGCTTTCAGTCTCTGTGGGATCGG	522
Db	520	GCACACAGATGCGCAAGGCGCGCTGAGACGCGCATTAATCAGTCTCTGTGGGATCGA	579
Qy	523	AACTTGGGCGAGGGGAAGCTCGGCCCCCTCCCAAGTGA	558
Db	580	AACTTGGGCGAAGAGGCTCCACCCCTTCCCAAGTGA	615

RESULT 10
 US-08-733-505A-15
 : Sequence 15, Application US/08733505A
 : Patent No. 5856445
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: KORSMEYER, STANLEY J.
 : TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
 : TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
 : NUMBER OF SEQUENCES: 60
 : CORRESPONDENCE ADDRESS:
 : ADDRESSER: HOWELL & HAFERKAMP, L.C.
 : STREET: 7733 FORSYTH BLVD., SUITE 1400
 : CITY: ST. LOUIS
 : STATE: MISSOURI
 : COUNTRY: USA
 :
 : ZIP: 63105
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/733,505A

APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSES: HOWELL & HAFFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-733-505A-17

Query Match 34.4%; Score 325.6; DB 2; Length 615;
Best Local Similarity 80.2%; Pred. No. 6.3e-74;
Matches 414; Conservative 0; Mismatches 84; Indels 18; Gaps 2;

QY 43 GCCCAGAGCAGTTCCTCAGATCCCAAGTTTGAAGCCGAGTGAAGCAGAGCAAGACTCCAGCTCT 102
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QY 103 GCAAGAGAGGGGCTGGGCCCCCGAGGGGAGCGGGCTCTCAGAGCTCCGGCAGAGCAT 162
DB 178 ACAAGTATAGGGGCTGGGCCCCCTGCTCAGTGAAGCAGCC-----AGGT 222
QY 163 CATGCCAGAGCCCGAGGCTCTGTTGGAGCGCCAGTCAACAGAGAGAGCAAGCCAGC 222
DB 223 CCCTACCTGAGCCCGAGGCTCTGTTGGAGCGCCAGTCAACAGAGAGAGCAAGCCAGC 282
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DB 343 GCGGGAGCGAGAGAGAGAGAGAGTGGGGAGAGAGCTTAAAGCTTTTTCAGAGAGGCTCG 402
QY 343 CGCTGGGGCGCCCAACCTCTGGGAGAGAGCGCTATAGCGCGGAGCTCCGAGAGATG 402
DB 403 CGTGGGGCTCCCCCAATCTCTGGGAGAGCGCGCTATAGCGCGGAGCTCCGAGAGATG 462
QY 403 AGTGAAGATTTGTGATCTCTTTAAGAGGAGCTTCTCGCCGAGAGAGCGGGGCA 462
DB 463 AGCGATGATTTGAAGGTTCTT-----CAAGGAGCTTCTCGCCCAAGAGCGCAGAGCACT 519
QY 463 GCAAGCGAGATGCGGCAAGCTCAGCTGAGAGCGAGTTCATCTCTGTTGGAGATG 522
DB 520 GCAACAGAGATGCGCAAGAGCGCGGCTGAGAGCGCATTTATCCAGTCTGTGGAGATG 579
QY 523 AACTTGGGAGAGGAGAGCTCCGCCCTCTCCAGTGA 558

DB 580 AACTTGGGAGAGGAGGCTCCAGCCCTCCAGTGA 615

RESULT 13
US-08-733-505A-18
Sequence 18, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSES: HOWELL & HAFFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-733-505A-18

Query Match 34.2%; Score 324; DB 2; Length 615;
Best Local Similarity 80.0%; Pred. No. 1.6e-73;
Matches 413; Conservative 0; Mismatches 85; Indels 18; Gaps 2;

QY 43 GCCCAGAGCAGTTCCTCAGATCCCAAGTTTGAAGCCGAGTGAAGCAGAGCAAGACTCCAGCTCT 102
DB 118 GCCCAGAGTATGTTCCAGATCCCAAGTTTGAAGCCGAGTGAAGCAGAGCAAGACTCCAGCTCT 177
QY 103 GCAAGAGAGGGGCTGGGCCCCCGAGGGGAGCGGGCTCTCAGAGCTCCGGCAGAGCAT 162
DB 178 ACAAGTATAGGGGCTGGGCCCCCTGCTCAGTGAAGCAGCC-----AGGT 222
QY 163 CATGCCAGAGCCCGAGGCTCTGTTGGAGCGCCAGTCAACAGAGAGAGCAAGCCAGC 222
DB 223 CCCTACCTGAGCCCGAGGCTCTGTTGGAGCGCCAGTCAACAGAGAGAGCAAGCCAGC 282
QY 223 AGCAGCATCATGAGAGCGCTGGGGCTGTGAGATCCCGAGTCCGCAACAGCTCTCAAGCC 282
DB 283 AACAGTCAATGAGAGCGCGCAGGGGCTATGAGACTCGGAGTCCGCAAGTTCTGATCCCA 342
QY 283 GCGGGAGCGAGAGAGAGAGAGTGGGGAGAGAGCCAGCCCTTTTGGGGCGGCTCG 342
DB 343 GCGGGAGCGAGAGAGAGAGAGTGGGGAGAGAGCTTAAAGCTTTTTCAGAGAGGCTCG 402
QY 343 CGCTGGGGCGCCCAACCTCTGGGAGAGAGCGCTATAGCGCGGAGCTCCGAGAGATG 402
DB 403 CGTGGGGCTCCCCCAATCTCTGGGAGAGCGCGCTATAGCGCGGAGCTCCGAGAGATG 462

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:20:29 ; Search time 1850 Seconds
(without alignments)
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Perfect score: 946

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Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Published Applications NA:*

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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	946	100.0	946	US-09-922-378-1	Sequence 1, Appl1
2	946	100.0	946	US-10-066-179-1	Sequence 1, Appl1
3	945	99.9	945	US-10-209-967-1	Sequence 1, Appl1
4	840.4	88.8	1105	US-09-894-657-2	Sequence 2, Appl1
5	799	84.5	953	US-09-873-367C-259	Sequence 259, App
6	400	42.3	477	US-09-918-995-27567	Sequence 27567, A
7	381.2	40.3	449	US-09-918-995-26409	Sequence 26409, A
8	344	36.4	1454	US-10-209-967-3	Sequence 3, Appl1
9	267.2	28.2	445	US-09-880-107-355	Sequence 355, App
10	211.4	22.3	303	US-09-783-590-4437	Sequence 3437, App
11	201.2	21.3	388	US-09-783-590-3465	Sequence 3465, App
12	175.6	18.6	235	US-09-833-381-166	Sequence 166, App
13	106.2	11.2	17580	US-10-240-452-12	Sequence 12, Appl
14	98.6	10.4	17580	US-10-240-452-11	Sequence 11, Appl
15	64.4	6.8	880	US-09-989-993-12	Sequence 12, Appl

16	60	6.3	60	US-09-908-975-13280	Sequence 13280, A
C 17	59.8	6.3	848	US-10-027-632-165125	Sequence 165125,
C 18	59.8	6.3	848	US-10-027-632-165125	Sequence 165125,
C 19	49.2	5.2	108	US-09-728-445-725	Sequence 725, App
C 20	43.4	4.6	3138	US-10-156-761-2538	Sequence 2538, App
C 21	43.4	4.6	9025608	US-10-156-761-1	Sequence 1, Appl1
C 22	43.2	4.6	4266	US-10-156-761-5083	Sequence 5083, App
C 23	43.2	4.6	9025608	US-10-156-761-1	Sequence 1, Appl1
C 24	42.2	4.5	143899	US-09-972-546-15	Sequence 15, Appl1
C 25	41.4	4.4	594	US-10-140-472-10	Sequence 10, Appl
C 26	41.4	4.4	594	US-10-141-761-10	Sequence 10, Appl
C 27	41.4	4.4	594	US-10-142-885-10	Sequence 10, Appl
C 28	41.4	4.4	594	US-10-158-790-10	Sequence 10, Appl
C 29	41.4	4.4	594	US-10-137-871-10	Sequence 10, Appl
C 30	41.4	4.4	594	US-10-140-805-10	Sequence 10, Appl
C 31	41.4	4.4	594	US-10-140-864-10	Sequence 10, Appl
C 32	41.4	4.4	594	US-10-140-823-10	Sequence 10, Appl
C 33	41.4	4.4	594	US-10-141-756-10	Sequence 10, Appl
C 34	41.4	4.4	594	US-10-141-759-10	Sequence 10, Appl
C 35	41.4	4.4	594	US-10-123-155-10	Sequence 10, Appl
C 36	41.4	4.4	594	US-10-146-731-10	Sequence 10, Appl
C 37	41.2	4.4	80557	US-10-080-170-647	Sequence 647, App
C 38	40.8	4.3	1036	US-10-140-472-142	Sequence 142, App
C 39	40.8	4.3	1036	US-10-141-761-142	Sequence 142, App
C 40	40.8	4.3	1036	US-10-142-885-142	Sequence 142, App
C 41	40.8	4.3	1036	US-10-158-790-142	Sequence 142, App
C 42	40.8	4.3	1036	US-10-137-871-142	Sequence 142, App
C 43	40.8	4.3	1036	US-10-140-805-142	Sequence 142, App
C 44	40.8	4.3	1036	US-10-140-864-142	Sequence 142, App
C 45	40.8	4.3	1036	US-10-140-923-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-09-922-378-1
Sequence 1, Application US/09922378
Patient No. US20020037869A1
GENERAL INFORMATION:
APPLICANT: Oltersdorf, Tilmann
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
FILE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922.378
CURRENT FILING DATE: 2001-08-03
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 946
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-378-1

Query Match 100.0%; Score 946; DB 9; Length 946;
Best Local Similarity 100.0%; Pred. NO. 8.2e-262;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGGCGTAAAGGGCGCGGTCAAGGGCTTCGAGATCGGGCTTGAGCCAGAGCATGTTCCAG	60
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QY	61	ATCCAGAGTTTGAAGCCAGAGGAGAGAGATCTTCAGACTTCGAGAGAGGGGCTTGAGC	120
DB	61	ATCCAGAGTTTGAAGCCAGAGGAGAGAGATCTTCAGACTTCGAGAGAGGGGCTTGAGC	120
QY	121	CCGAGCCCGGAGAGGAGAGGAGGCTTCAGAGCTTCGAGAGAGATTCGAGAGGAGGAGG	180
DB	121	CCGAGCCCGGAGAGGAGAGGAGGCTTCAGAGCTTCGAGAGAGATTCGAGAGGAGGAGG	180
QY	181	CTCCTGTGGAAGGCGAGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	240
DB	181	CTCCTGTGGAAGGCGAGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	240

D	b	1	b1	CTCTGTGGAGCGCAGTACACAGGAGGAGCAGCACCACAGACGAGCATATGAGGC	240
O	y	2	21	GCTGGGCGTGTGAGAGTCCGGAAGTCGCACAGCTCTACCCCGCGGGGACGGAGAGAC	3000
D	b	2	241	GCTGGGGCGTGTGAGAGTCCGGAAGTCGCACAGCTCTACCCCGCGGGGACGGAGAGAC	3000
O	y	3	301	GAAGGAGATGGGGGAGGAGGCCAGGCCCTTTCCGGGGCGGCTCGGAGCTCGGCGCCCAAC	3600
D	b	3	301	GAAGGAGATGGGGGAGGAGGCCAGGCCCTTTCCGGGGCGGCTCGGAGCTCGGCGCCCAAC	3600
O	y	3	361	CTCTGGGACGACAGCGCTATGGCCCGAGAGCTTCGAGAGATGATGACAGATTTGTGAC	4200
D	b	3	361	CTCTGGGACGACAGCGCTATGGCCCGAGAGCTTCGAGAGATGATGACAGATTTGTGAC	4200
O	y	4	421	TCCTTTAAGAGAGGACTTCTCGGCCGAAAGAGCGCGGACACAGCAACGACGATGCGGCA	4800
D	b	4	421	TCCTTTAAGAGAGGACTTCTCGGCCGAAAGAGCGCGGACACAGCAACGACGATGCGGCA	4800
O	y	4	481	AGCTCCAGCTGAGACGGAGATCTTCCAGCTCGTGGGATTCGGAACTTTGGCAGAGGAAAC	5400
D	b	4	481	AGCTCCAGCTGAGACGGAGATCTTCCAGCTCGTGGGATTCGGAACTTTGGCAGAGGAAAC	5400
O	y	5	541	TCGCGCCCCCTCCAGTGAACCTTCGATCCACATCCGAAATCCACCGGTTCCATTGCCCT	6000
D	b	5	541	TCGCGCCCCCTCCAGTGAACCTTCGATCCACATCCGAAATCCACCGGTTCCATTGCCCT	6000
O	y	6	601	GGGACGCCATTTTGAATATGGAGGAGTAGTAGTTCCCTCAGGCTATGCAAAAAAGAGAT	6600
D	b	6	601	GGGACGCCATTTTGAATATGGAGGAGTAGTAGTTCCCTCAGGCTATGCAAAAAAGAGAT	6600
O	y	6	661	CCGTGCTGATCCTTTGGAGGAGGAGTTGACCCAGATTCCCTTCGGTGTGTGAAGCC	7200
D	b	6	661	CCGTGCTGATCCTTTGGAGGAGGAGTTGACCCAGATTCCCTTCGGTGTGTGAAGCC	7200
O	y	7	721	ACGGAAGGTGGTCCCATGGGAAGTTTGGGTTTCCGCCACAGCGCGCGGAAGTGGCT	7800
D	b	7	721	ACGGAAGGTGGTCCCATGGGAAGTTTGGGTTTCCGCCACAGCGCGCGGAAGTGGCT	7800
O	y	7	781	CCGTGGCCCGGCTCAGGTTCCCGGGGTTTCCCGACAGCGCTCGCGTAAGTACGAGCC	8400
D	b	7	781	CCGTGGCCCGGCTCAGGTTCCCGGGGTTTCCCGACAGCGCTCGCGTAAGTACGAGCC	8400
O	y	8	841	AGGTTTAACCGTTGTGTCAACGGGACCCGAGCCCGCGCATGCTGTGGGGCGGTGATCA	9000
D	b	8	841	AGGTTTAACCGTTGTGTGTCAACGGGACCCGAGCCCGCGCATGCTGTGGGGCGGTGATCA	9000
O	y	9	901	GTAACCAAAATGTTAATAAGCCCGCGGTGTGCCAAAAAAGAGAGAGAGAGAGAGAGAG	946
D	b	9	901	GTAACCAAAATGTTAATAAGCCCGCGGTGTGTGCCAAAAAAGAGAGAGAGAGAGAGAGAG	946

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RESULT 2
US-10-066-179-1
; Sequence 1, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-179-1

Query Match      100.0%;      Score 946;  DB 14;      Length 946;
Best Local Similarity 100.0%;      Pred. No. 8.2e-262;

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Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY		GGGCTTAGGGCCGCGGGGTCAAGGAGCCTGAAATCGAGCTTGTGGGCCAGAGCATTTTCAG	60
Db	1	GGGCTTAGGGCCGCGGGGTCAAGGAGCCTGAAATCGAGCTTGTGGGCCAGAGCATTTTCAG	60
QY		ATCCAGAGTTTGAGCCGAGTGAGCAGGAAAGCTTCAGCTCTGCAAGAGAGGGGCTTG	120
Db	61	ATCCAGAGTTTGAGCCGAGTGAGCAGGAAAGCTTCAGCTCTGCAAGAGAGGGGCTTG	120
QY		CCCAAGCCCGCAGAGGAGCGGGGCCCTCAGGCTCCGGCAAGCATCATTCGCGAGCCCA	180
Db	121	CCCAAGCCCGCAGAGGAGCGGGGCCCTCAGGCTCCGGCAAGCATCATTCGCGAGCCCA	180
QY		CTCCGTGGGAGCGCCAGTCAACAGCAGGAGCAGCAACACAGCAGAGCATCATGAGAGC	240
Db	181	CTCCGTGGGAGCGCCAGTCAACAGCAGGAGCAGCAACACAGCAGAGCATCATGAGAGC	240
QY		CTCTCTGTGGAGCGCCAGTCAACAGCAGGAGCAGCAACACAGCAGAGCATCATGAGAGC	300
Db	241	CTCTCTGTGGAGCGCCAGTCAACAGCAGGAGCAGCAACACAGCAGAGCATCATGAGAGC	300
QY		GCTGGGGCTGTGGAGATCCGAGTGCACAGACTCTACCCCGCGGGGACGAGAGCAGC	360
Db	301	GCTGGGGCTGTGGAGATCCGAGTGCACAGACTCTACCCCGCGGGGACGAGAGCAGC	360
QY		GAAGGAGTGGGGGAGAGAGCCAGCCCTTTTCGGGGCGCTGCGCTCGCGCCCTCCAC	420
Db	361	GAAGGAGTGGGGGAGAGAGCCAGCCCTTTTCGGGGCGCTGCGCTCGCGCCCTCCAC	420
QY		CTCTGGGACAGCAGAGGCTATGAGCGCGAGCTCCGAGAGATGAGTGAAGATTTGTGAC	480
Db	421	CTCTGGGACAGCAGAGGCTATGAGCGCGAGCTCCGAGAGATGAGTGAAGATTTGTGAC	480
QY		TCCTTTAAGAGGAGCTTCTCGCCGAGAGCGCGGACAGCAGCAACGAGATCGGCA	540
Db	481	TCCTTTAAGAGGAGCTTCTCGCCGAGAGCGCGGACAGCAGCAACGAGATCGGCA	540
QY		AGCTCCAGCTGAGCGGAGTCTTCCAGTCTGTGTGGATCGGAACTTGGGACGGGAAAC	600
Db	541	AGCTCCAGCTGAGCGGAGTCTTCCAGTCTGTGTGGATCGGAACTTGGGAGCGGAAAC	600
QY		TCGCGCCCTCCGAGTGAACCTTTCGATCCAGTCCGAAATCAACCTGTTCCATTTGCC	660
Db	601	TCGCGCCCTCCGAGTGAACCTTTCGATCCAGTCCGAAATCAACCTGTTCCATTTGCC	660
QY		GGGAGGCAATTTTGAATATGGAGGAGTAAATTCCTCAGAGCTATGCAAAAAGAGAT	720
Db	661	GGGAGGCAATTTTGAATATGGAGGAGTAAATTCCTCAGAGCTATGCAAAAAGAGAT	720
QY		CCGTGCTGTAATCTTTGAGGAGGAGTGAACCAATTCCTTCCGTTGTGTGAAGCC	780
Db	721	CCGTGCTGTAATCTTTGAGGAGGAGTGAACCAATTCCTTCCGTTGTGTGAAGCC	780
QY		ACGGAAGGTGTGCCATCGAAAGTTTGGTTTTCCGCCACAGCGCCGGAAGTGGCT	840
Db	781	ACGGAAGGTGTGCCATCGAAAGTTTGGTTTTCCGCCACAGCGCCGGAAGTGGCT	840
QY		CCGTGAGCCCGCCTCAGGTTCCGGGAGTTTCCCCAGGAGGCTGCGTAAATGAGAGCC	900
Db	841	CCGTGAGCCCGCCTCAGGTTCCGGGAGTTTCCCCAGGAGGCTGCGTAAATGAGAGCC	900
QY		AGGTTTAAACGTTGTGTCAACCGGAGACCGAGCCCCCGGAGAGCCTTGCGGCGCTGATCA	960
Db	901	AGGTTTAAACGTTGTGTGTCAACCGGAGACCGAGCCCCCGGAGAGCCTTGCGGCGCTGATCA	960
QY		GTACCAAATGTATAAAGCCCGCGTGTGCAAAAAAAGAAAAA 946	
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RESULT 3
US-10-209-967-1
; Sequence 1, Application US/10209967
; Publication No. US20030171279A1
; GENERAL INFORMATION:
; APPLICANT: MUNGER, JOSHUA

QY	103	CAAGAGAGGGGCTTGGGGCCCAAGCCCGGAGGGGAACTGGGCGCTCAGAGCTCCGGCAAGACT	162
Db	265	GCAGAGAGGGGCTTGGGGCCCAAGCCCGGAGGGGAACTGGGCGCTCAGAGCTCCGGCAAGACT	324
QY	163	CATGCGCAGGCGCCAGAGGCTCTGTGTGGACGCGCAGTCACACAGAGAGGACGCCAACAGC	222
Db	325	CATGCGCAGGCGCCCAAGGCTCTGTGTGGACGCGCAGTCACACAGAGAGGACGCCAACAGC	384
QY	223	AGCAGCCATCATGTAGAGGGCGTGGGGCTGTGTGAGATCCGGGAGTCGCCACAGCTCTTACCCC	282
Db	385	AGCAGCCATCATGTAGAGGGCGTGGGGCTGTGTGAGATCCGGGAGTCGCCACAGCTCTTACCCC	444
QY	283	GCGGGGACGAGAGACGACGAAAGGATGAGGGGAGAGAGCCAGCCCTTTGAGGGGCGCTCG	342
Db	445	GCGGGGACGAGAGACGACGAAAGGATGAGGGGAGAGAGCCAGCCCTTTGAGGGGCGCTCG	504
QY	343	CGCTTGGGGCCCCCCTTCTGTGGGACGACACAGCGCTATGTGCGCGGACGCTCCGAGAGATG	402
Db	505	CGCTTGGGGCCCCCCTTCTGTGGGACGACACAGCGCTATGTGCGCGGACGCTCCGAGAGATG	564
QY	403	AGTAGCAGATTGTGTGACCTCTTTAAGAGGGACCTTCTCGCCCCAAGAGACGGGGACAC	462
Db	555	AGTAGCAGATTGTGTGACCTCTTTAAGAGGGACCTTCTCGCCCCAAGAGACGGGGACAC	624
QY	463	GCAACGCAGATGCGGCAAAAGCTCCAGCTGACGCGAGTCCTTCCAGTCTGTGTGGATCGG	522
Db	625	GCAACGCAGATGCGGCAAAAGCTCCAGCTGACGCGAGTCCTTCCAGTCTGTGTGGATCGG	684
QY	523	AACTTGGGCGAGGGGAAAGCTCCGGCCCCCTCCCAAGTACCTTCGGTCCACATCCCGAAATTC	581
Db	685	AACTTGGGCGAGGGGAAAGCTCCGGCCCCCTCCCAAGTACCTTCGGTCCACATCCCGAAATTC	744
QY	582	CACCGGTTCCCATTTGCGCTCGGACAGCCATTTTGAAATATGGAAGAGTAATGTTCCCTCAG	641
Db	745	CACCGGTTCCCATTTGCGCTCGGAGAGCCATTTTGAAATATGGAAGAGTAATGTTCCCTCAG	803
QY	642	GGCTATGCAAAAAGAGATCCGCTGCTGTATCCTTTGGAAGGAGGGTTGACCCAGATTTCC	701
Db	804	GGCTATGCAAAAAGAGATCCGCTGCTGTATCCTTTGGAAGGAGGGTTGACCCAGATTTCC	863
QY	702	TTCCGGTGTGTGAAAGCCAGCGAAAGG-TTGGTCCCATCGGAAATTTTGGGTTTTCGCGC	760
Db	864	TTCCGGTGTGTGAAAGCCAGCGAAAGGCTTGGTCCCATCGGAAATTTTGGGTTTTCGCGC	923
QY	761	CACAGCCCGCGGAAGTGCGTCCGTGGCGCCCGCCTCAGGTTCCGGGGATTTCCCCAGGCG	820
Db	924	CACAGCCCGCGGAAGTGCGTCCGTGGCGCCCGCCTCAGGTTCCGGGGATTTCCCCAGGCG	983
QY	821	CCTGGGCTTAAGTAAAGGAGCGAGGTTTAAACGTTGTCTACCGGGGACCCGAGCCCGCGA	880
Db	984	CCTGGGCTTAAGTAAAGGAGCGAGGTTTAAACGTTGTCTACCGGGGACCCGAGCCCGCGA	1044
QY	881	TGCGCTGGGGGCGCGTGATCAGTACCAATGTTATATTAAGCCCGCGTGTGTGCCAAAAAAA	940
Db	1044	TGCGCTGGGGGCGCGTGATCAGTACCAATGTTATATTAAGCCCGCGTGTGTGCCAAAAAAA	1104
QY	941	AA 942	
Db	1104	AA 1105	

	TITLE OF INVENTION: Signature Gene Sets	
	FILE REFERENCE: 689290-64	
	CURRENT APPLICATION NUMBER: US/09/873.367C	
	CURRENT FILING DATE: 2003-04-29	
	PRIOR APPLICATION NUMBER: U.S. 60/236,891	
	PRIOR FILING DATE: 2000-09-29	
	PRIOR APPLICATION NUMBER: U.S. 60/236,842	
	PRIOR FILING DATE: 2000-09-29	
	PRIOR APPLICATION NUMBER: U.S. 60/244,867	
	PRIOR FILING DATE: 2000-11-01	
	PRIOR APPLICATION NUMBER: U.S. 60/245,084	
	PRIOR FILING DATE: 2000-11-01	
	NUMBER OF SEQ ID NOS: 1067	
	SOFTWARE: PatentIn version 3.0	
	SEQ ID NO 259	
	LENGTH: 953	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	US-09-873-367C-259	
Query Match	84.5%; Score 799; DB 13; Length 953;	
Best Local Similarity	97.7%; Pred. No. 1.4e-219;	
Matches 874; Conservative	0; Mismatches 15; Indels 6; Gaps 6;	
Oy	43 GCCGAGACGAATGCCAGATCCCGAAGTTTAAAGCGAGTGAGCAAGGAGACTCCAGCTC	102
Dd		
Oy	58 GCCGAGACGAATGCCAGATCCCGAAGTTTAAAGCGAGTGAGCAAGGAGACTCCAGCTC	117
Oy	103 GCAGAAGAGGGCCCTGGGCCCCAGCCCAGCGGAGCAAGGAGCCCTCAGCTCCGACAAAGCAT	162
Dd	118 GCAGAAGAGGGCCCTGGGCCCCAGCCCAGCGGAGCAAGGAGCCCTCAGCTCCGACAAAGCAT	177
Oy	163 CATGCCACAGCCCCAGGCTTCCTGTGGAGCCCAAGTCACACGACGAGAGCAAGCAACCAACC	222
Dd	178 CATGCCACAGCCCCAGGCTTCCTGTGGAGCCCAAGTCACACGAGTAGAGCAAGCAAGTCCTAAC	237
Oy	223 AGCAGGCATATATGAGAG-CGCTGGGGCTGTGTGAATCCGGAGTGCCACAGTCTCTAAC	281
Dd	238 AGCAGGCATATATGAGAGCGCTGGGGCTGTGTGAATCCGGAGTGCCACAGTCTCTAAC	297
Oy	282 CGCGAGGAGCGAGAGCAAGCAAGGAGATGGGGAGAGAGCCCAAGCCCTTCGAGGCGGCTC	341
Dd	298 CGCGAGGAGCGAGAGCAAGCAAGGAGATGGGGAGAGAGCCCAAG-CCTTCGAGGCGGCTC	356
Oy	342 GCGCTCGGCGCCCCCAAACCTCTGGGAGCACAGCGCTTATGAGCGCGAGCTCCGAGGAT	401
Dd	357 GCGCTCGGCGCCCCCAAACCTCTGGGAGCACAGCGCTTATGAGCGCGAGCTCCGAGGAT	416
Oy	402 GAGTGAAGCATTTGTGACCTCTTTAAGAAAGGACTTCTCGCCCCGAAGAGAGCGGAGCAC	461
Dd	417 GAGTGAAGCATTTGTGACCTCTTTAAGAAAGGACTTCTCGCCCCGAAGAGAGCGGAGCAC	476
Oy	462 AGCAACGAGATGCGGCAAAAGCTCAGCTGAGCGGAGTCTTCCAGTCTCTGGTGGGATCG	521
Dd	477 AGCAACGAGATGCGGCAAAAGCTCAGCTGAGCGGAGTCTTCCAGTCTCTGGTGGGATCG	536
Oy	522 GAACCTGGGAGGAGGAAGCTCGCCCTCCCAAGTCACTTCGATCCAATCCGAAA-T	580
Dd	537 GAACCTGGGAGGAGGAAGCTCGCCCTCCCAAGTCACTTCGATCCAATCCGAAA-T	596
Oy	581 CCACCCGTTCCCATTTGCTTGGGAGCAATTGTAATATGGGAGGAAATAAGTTTCCCTCA	640
Dd	597 CCACCCGTTCCCATTTGCTTGGGAGCAATTGTAATATGGGAGGAAATAAGTTTCCCTCA	655
Oy	641 GGCCATATCAAAAAAGAGATCCGATGCTATCTTTGGAGGAGGAGGTTGACCCAGATTCC	700
Dd	656 GGCCATATCAAAAAAGAGATCCGATGCTATCTTTGGAGGAGGAGGTTGACCCAGATTCC	715
Oy	701 CTTCCGATGTGTGAAGCCAGGAGG-TTGATCCCATCGAAATTGATTTTCGCG	759
Dd	716 CTTCCGATGTGTGAAGCCAGGAGGCTTGATCCCATCGAAATTGATTTTCGCG	775
Oy	760 CCAAGCCCGGAGATGGCTTCGATGCGCCGCTCAGGTTCCGGGATTTTCCCAAGGC	819

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Db      776 CCAAGACCCCGGAGAGTGGCTCGTGGCCCGCCCTCAGGCTCCGGGCTTTCCCGCAGGC 835
Qy      820 GCGTGGCTAAGTAGAGGAGCCAGTTTACCGTGTGTACCGGGAGCCGAGCCCGCCGG 879
Db      836 GCGTGGCTAAGTAGAGGAGCCAGTTTACCGTGTGTACCGGGAGCCGAGCCCGCCGG 895
Qy      880 ATGCCCTGGGGG-CGCTGATCAGTACCAATGTTAATAAGCCCGGCTGTGCC 933
Db      896 ATGCCCTGGGGGCGCTGTCTACTACCAATGTTAATAAGCCCGGCTGTGCC 950

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RESULT 6

US-09-918-995-27567
 ; Sequence 27567, Application US/09918995
 ; Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: HySeq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 27567

LENGTH: 477

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(477)

OTHER INFORMATION: n = A,T,C or G

US-09-918-995-27567

Query Match 42.3% Score 400; DB 11; Length 477;

Best Local Similarity 97.4%; Pred. No. 5.4e-105;

Matches 406; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy      34 CCGGCTTGGGCCAGAGCATGTTCCAGATCCAGAGTTTGAAGCCGAGTAGAGAGAGAGC 93
Db      61 CCGGCTTGGGCCAGAGCATGTTCCAGATCCAGAGTTTGAAGCCGAGTAGAGAGAGC 120
Qy      94 TCCAGCTTGCAGAGAGGGGCTGGGCCCGCAGCGCCGAGGGAGGGGCTTCAAGCTCC 153
Db      121 TCCAGCTTGCAGAGAGGGGCTGGGCCCGCAGCGCCGAGGGAGCTGCTCATGCTTC 180
Qy      154 GGCAGAGCATGAGCGAGGCCCGCAGGCTCTGTGGAGGCGCAGTCCAGAGAGAGAGC 213
Db      181 GGCAGAGCATGAGCGAGGCCCGCAGGCTCTGTGGAGGCGCAGTCCAGAGAGAGAGC 240
Qy      214 CCAACAGAGAGCATGAGTGAAGGCGCTGGAGCTGTGAGATCCGAGTCCAGCAGC 273
Db      241 CCAACAGAGAGCATGAGTGAAGGCGCTGGAGCTGTGAGATCCGAGTCCAGCAGC 300
Qy      274 TCTTACCCCGGGGAGCGAGAGCAGAGGAGTGGGGAGAGGCCAGCCCTTTTGG 333
Db      301 TCTTACCCCGGGGAGCGAGAGCAGAGGAGTGGGGAGAGGCCAGCCCTTTTGG 360
Qy      334 GGCAGCTGGCGCTGGGGCGCCCGCAGACCTCTGGGAGCAGCGCTATGCGCGAGCTC 393
Db      361 GGCAGCTGGCGCTGGGGCGCCCGCAGACCTCTGGGAGCAGCGCTATGCGCGAGCTC 420
Qy      394 CGAGAGTAGTAGAGAGTGTGTGAGCTCTTTAAGAGGAGCTTCTGCGCCGAG 450
Db      421 CGAGAGTAGTAGAGAGTGTGTGAGCTCTTTAAGAGGAGCTTCTGCGCCGAG 477

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RESULT 7

US-09-918-995-26409

; Sequence 26409, Application US/09918995

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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 26409
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26409

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Query Match 40.3% Score 381.2; DB 11; Length 449;

Best Local Similarity 97.6%; Pred. No. 1.3e-99;

Matches 408; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

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Qy      297 CGACGAAGAGTAGGGGAGAGAGCCGAGCCCTTGGGGGCGCTGCGCGGCGCC 356
Db      32 CGACGAAGAGTAGGGGAGAGAGCCGAGCCCTTGGGGGCGCTGCGCGGCGCC 91
Qy      357 CAACCTTGGGAGAGAGAGCCCTATGCGGAGCTCCGAGAGTAGAGTAGATTGT 416
Db      92 CAACCTTGGGAGAGAGAGCCCTATGCGGAGCTCCGAGAGTAGAGTAGATTGT 151
Qy      417 GCACTCTTTAAGAGGAGCTTCTGCGGAGAGGCGGAGCAGAGCAGAGATCG 476
Db      152 GCACTCTTTAAGAGGAGCTTCTGCGGAGAGGCGGAGCAGAGCAGAGATCG 211
Qy      477 GCAAGCTCCAGCTGAGAGCGAGTTCAGTCTCTGAGGAGTGGAACTGGGGAGGG 536
Db      212 GCAAGCTCCAGCTGAGAGCGAGTTCAGTCTCTGAGGAGTGGAACTGGGGAGGG 271
Qy      537 AAGCTCGGCCCTCCAGTAGCTTGGTCCATCCGAAA-TCCAGCCGTTCCATT 595
Db      272 AAGCTCGGCCCTCCAGTAGCTTGGTCCATCCGAAA-TCCAGCCGTTCCACT 331
Qy      596 GCCCTGGCAGCCATTGTAATATGAGAGAGTAAGTTCCCTCAGGCTATGCAAAAAG 655
Db      332 GCCCTGGCAGCCATTGTAATATGAGAGAGT-ATTCCCTCAGGCTATGCAAAAAG 390
Qy      656 AGATCCGTGCTGATCTTTTGAAGAGAGGTTGACCAAGTCCCTTCCGCTGTG 713
Db      391 AGATCCGTGCTGCTCTCTTTGAGAGGAGGCTGACCAAGTCCCTTCCGCTGTG 448

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RESULT 8

US-10-209-967-3

; Sequence 3, Application US/10209967

; Publication No. US20030171279A1

GENERAL INFORMATION:

APPLICANT: MÜNGER, JOSHUA

TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND

FILE REFERENCE: ARCD:380US

CURRENT APPLICATION NUMBER: US/10/209,967

PRIOR FILING DATE: 2002-07-31

PRIOR APPLICATION NUMBER: 60/308,929

PRIOR FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 3

LENGTH: 1454

TYPE: DNA
ORGANISM: Mus musculus
US-10-209-967-3

Query Match 36.4%; Score 344; DB 13; Length 1454;
Best Local Similarity 76.9%; Pred. No. 7.8e-89;
Matches 480; Conservative 0; Mismatches 120; Indels 24; Gaps 4;

43 GCCCAGACATGTTCCAGATCCAGAGTTTGAAGCCAGATGAGCAGAGAGACTCCAGCTCT 102
Db GCCCAGACATGTTCCAGATCCAGAGTTTGAAGCCAGATGAGCAGAGAGACTCCAGCTCT 647
Qy 588 GCCCAGACATGTTCCAGATCCAGAGTTTGAAGCCAGATGAGCAGAGAGACTCCAGCTCT 647
Qy 103 GCAAGAGAGGCTCTGAGGCTCCAGAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 162
Db 648 ACAGATAGGAGGCTCTGAGGCTCCAGAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 692
Qy 163 CATGCGCAGGCTCCAGAGCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 222
Db 693 CCTACCTGAGGCTCCAGAGCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 752
Qy 223 AGCAGCATCATGAGAGGCTGAGGCTGAGAGATCCAGAGTCCAGAGCTCCAGAGCTCC 282
Db 753 AACGATCATGAGAGGCTGAGGCTGAGAGATCCAGAGTCCAGAGCTCCAGAGCTCCAGAGCT 812
Qy 283 GCGGAG 342
Db 813 GCGGAG 872
Qy 343 GCGTGGGAG 402
Db 873 GGTGGGAG 932
Qy 403 AGTGCAGATGTTGAGATCTCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
Db 933 AGCAGATGTTGAG 989
Qy 463 GCAACGAGATGCGGAG 522
Db 990 GCAACAGATGCGGAG 1049
Qy 523 AACTTGGGAG 581
Db 1050 AACTTGGGAG 1107
Qy 582 CACCGGTTCCAGATGCTCTGAG 641
Db 1108 ---CTTACCGGCTCCAG 1164
Qy 642 GCTATGCAAAAGAGATCCGTG 665
Db 1165 TAGGAAAAAAGAGATCCGTG 1188

RESULT 9
US-09-880-107-355/c
Sequence 355, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Voelckley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-MO
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 355

LENGTH: 445
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA160775
NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: n = a or c or g or t
US-09-880-107-355

Query Match 28.2%; Score 267.2; DB 10; Length 445;
Best Local Similarity 88.5%; Pred. No. 7.6e-67;
Matches 401; Conservative 0; Mismatches 38; Indels 14; Gaps 10;

Qy 493 ACCGAGTCTTCCAGTCTCTGAGAGATCGAAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
Db 445 ACCGAGTCTTCCAGTCTCTGAGAGATCGAAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 390
Qy 553 CAGTGAACCTTGGTCCATCCGAAA--TCACCCGTTCCATGCTCTGGGAGGAGAT 610
Db 389 CAGTGAACCTTGGTCCATCCGAAA--TCACCCGTTCCATGCTCTGGGAGGAGAT 330
Qy 611 TTGAAATATGAG 668
Db 329 CTGAAATATGAG 270
Qy 669 TATCCTTTGAG 727
Db 269 TCTCTTTGAG 210
Qy 728 G-TTGTCCATCGAAGTTTGGGTTTCCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
Db 209 GCTTGTCCATCGAAGTTTGGGTTTCCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 151
Qy 787 CCCCCCTTCAAGTCTCCGAGGTTTCCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
Db 150 -CCACNCTTCAAGTCTCCGAGGTTTCCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 93
Qy 847 AACGTTGTCAACCGGAG 906
Db 92 AACGTTGTCAACCGGAG 34
Qy 907 AATGTTAATAAGCCGCTGTGTGCAAAAA 939
Db 33 AATGTTAATAAGCCGCTGTGTGCAAAAA 1

RESULT 10
US-09-783-590-3437
Sequence 3437, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT FILING DATE: 2000-02-15
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1994-11-21
PRIOR APPLICATION NUMBER: 08/346,731
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3437
LENGTH: 303
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature


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/ LOCATION: (165)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (173)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (187)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (193)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (236)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (246)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (251)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (280)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (281)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (289)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (303)
/ OTHER INFORMATION: n equals a,t,g, or c
/ US-09-783-590-3437

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Query Match      22.3%; Score 211.4, DB 10; Length 303;
Best Local Similarity 88.5%; Pred. No. 7.7e-51;
Matches 269; Conservative 0; Mismatches 30; Indels 5; Gaps 4;

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QY 402 GAGTACGAGTTGTGGACCTCTTAAGAGGAGCTCCCGCCGAGAGCGCGGGCAGC 461
DB 1 GAGTACGAGTTGTGGACCTCTTAAGAGGAGCTCCCGCCGAGAGCGCGGGCAGC 60
QY 462 AGCAAGCAGATGCGGCAAGCTCCAGCTGG-ACGGAGCTCCAGTCCCTGGTGGATC 520
DB 61 AGCAAGCAGATGCGGCAAGCTCCAGCTGGAGCGAGCTCCAGTCCCTGGTGGATC 120
QY 521 GGAATTGGGCGAGGAGGAGCTCCGCGCCCTCCCAAGTGAACCTTGCATCCGGAAT 580
DB 121 GGAATTGGGCGAGGAGGAGCTCCGCGCCCTCCCAAGTGAACCTTGCATCCGGAAT 180
QY 581 CCACCCGTTCCATTGCCCTGGGAGCAGCATTTGATATGGAGAGTAAGTCCCTCA 640
DB 181 TCACCCGTTCCATTGCCCTGGGAGCAGCATTTGATATGGAGAGTAAGTCCCTCA 237
QY 641 GGCCTATGCAAAAAGAGATCCGTGCTGTATCCTTTGAGAGG-AGGATGACCCAGATTC 699
DB 238 GGCCTATGCAAAAAGAGATCCGTGCTGTATCCTTTGAGAGGAGGAGTTCATTTT 297
QY 700 CCTT 703
DB 298 CCTT 301

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RESULT 11
US-09-783-590-3465
/ Sequence 3465, Application US/09783590
/ Patent No. US20020110850A1
/ GENERAL INFORMATION:
/ APPLICANT: Dillon, Patrick J.
/ APPLICANT: Haseltine, William A.
/ APPLICANT: Li, Haodong
/ APPLICANT: Rosen, Craig A.
/ APPLICANT: Ruben, Steven M.

```

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/ TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
/ FILE REFERENCE: PO-16.2C1
/ CURRENT APPLICATION NUMBER: US/09/783,590
/ CURRENT FILING DATE: 2000-02-15
/ PRIOR APPLICATION NUMBER: 08/420,856
/ PRIOR FILING DATE: 1995-04-12
/ PRIOR APPLICATION NUMBER: 08/346,731
/ PRIOR FILING DATE: 1994-11-21
/ NUMBER OF SEQ ID NOS: 12485
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 3465
/ LENGTH: 388
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (76)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (92)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (104)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (279)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (324)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (352)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (355)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (363)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (376)
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/ NAME/KEY: misc feature
/ LOCATION: (377)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc feature
/ LOCATION: (385)
/ OTHER INFORMATION: n equals a,t,g, or c
/ US-09-783-590-3465

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Query Match      21.3%; Score 201.2, DB 10; Length 388;
Best Local Similarity 86.9%; Pred. No. 6.8e-48;
Matches 278; Conservative 0; Mismatches 35; Indels 7; Gaps 5;

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QY 402 GAGTACGAGTTGTGGACCTCTTAAGAGGAGCTCCCGCCGAGAGCGCGGGCAGC 461
DB 1 GAGTACGAGTTGTGGACCTCTTAAGAGGAGCTCCCGCCGAGAGCGCGGGCAGC 60
QY 462 AGCAAGCAGATGCGGCAAGCTCCAGCTGG-ACGGAGCTT-CCAGTCCGTGGAT 519
DB 61 AGCAAGCAGATGCGGCAAGCTCCAGCTGGAGCGAGTCTTNCAGTCCGTGGAT 120
QY 520 CGGAATTGGGCGAGGAGGAGCTCCGCGCCCTCCCAAGTGAACCTTGCATCCGGA 577
DB 121 CGGAATTGGGCGAGGAGGAGCTCCGCGCCCTCCCAAGTGAACCTTGCATCCGGA 180
QY 578 AA-TCCACCCGTTCCATTGCCCTGGGAGCAGCATTTGATATGGAGAGTAAGTTC 636
DB 181 AACTCACCCGTTCCATTGCCCTGGGAGCAGCATTTGATATGGAGAGTAAGTTC 240
QY 637 CTCAGGCTATGCAAAAAGAGATCCGTGCT--GTATCCTTTGAGAGGAGGTTGACCA 694
DB 241 CTCAGGCTATGCAAAAAGAGATCCGTGCTGCTTCTTGGGAGGAGGTTGACCA 300

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100

QY 227 GCCATCATGAGG 239
DB 5176 GTTATTATGAGG 5188

RESULT 15

US-09-989-993-12/c
; Sequence 12, Application US/09989993
; Publication No. US20030134263A1
; GENERAL INFORMATION:
; APPLICANT: Erives, Albert
; TITLE OF INVENTION: REGULATORY NUCLEIC ACID ASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC AND LIBRARY SCREENS
; FILE REFERENCE: 52400-20002.00
; CURRENT APPLICATION NUMBER: US/09/989,993
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12
; LENGTH: 880
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-989-993-12

Query Match 6.8%; Score 64.4; DB 13; Length 880;
Best Local Similarity 86.6%; Pred. No. 1.5e-08;
Matches 71; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 366 GGCACACAGCGCCTATGCGCGGAGCTCCGAGATGACGATTGTGACTCCTT 425
DB 880 GGCACACAGCGCCTATGCGCGGAGCTCCGAGATGACGATTGTGACTCCTT 821
QY 426 TAAGAAGGAGCTTCTCGCCCG 447
DB 820 TAGGTGAGCGCCAGTCCCCAG 799

Search completed: December 29, 2003, 23:29:39
Job time : 1870 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 29, 2003, 15:12:07 ; Search time 19244 Seconds
(without alignments)
1630.271 Million cell updates/sec

Title: US-10-066-179-1

Perfect score: 946

Sequence: 1 99gcctagggcgccggtca.....gtgtgcaaaaaaaaaa 946

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	946	100.0	946	20	US-09-376-154-1
2	946	100.0	946	39	US-09-922-378-1
3	946	100.0	946	45	US-10-066-179-1
4	945	99.9	945	48	US-10-209-967-1

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5 871.2 92.1 1006 28 US-09-652-916-9142 Sequence 9142, Ap
6 871.2 92.1 1006 28 US-09-652-917-3158 Sequence 3158, Ap
7 871.2 92.1 1006 30 US-09-699-997-10996 Sequence 10996, A
8 871.2 92.1 1006 32 US-09-726-787-2372 Sequence 2372, Ap
9 871.2 92.1 1006 32 US-09-726-809-2815 Sequence 2815, Ap
10 861.4 91.1 962 31 US-09-705-256A-5838 Sequence 5838, Ap
11 861.4 91.1 962 70 US-60-164-285-5838 Sequence 5838, Ap
12 840.4 88.8 1105 37 US-09-894-657-2 Sequence 2, Appl1
13 839.2 88.7 1143 71 US-60-172-373-13906 Sequence 13906, A
14 839.2 88.7 1143 82 US-60-278-258-16973 Sequence 16973, A
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16 833 88.1 1127 2 PCT-US03-07713-369 Sequence 369, App
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18 833 88.1 1127 96 US-60-412-049-369 Sequence 369, App
19 831.6 87.9 1343 32 US-09-758-466-233 Sequence 233, App
20 831.6 87.9 1343 48 US-10-232-809-233 Sequence 233, App
21 799 84.5 953 13 US-08-883-731-1 Sequence 1, Appl1
22 799 84.5 953 13 US-08-883-731-3 Sequence 3, Appl1
23 799 84.5 953 15 US-09-053-375B-1231 Sequence 1231, Ap
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25 799 84.5 971 15 US-09-023-655-646 Sequence 646, App
26 799 84.5 971 53 US-10-641-643-646 Sequence 646, App
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29 546 57.7 842 49 US-10-264-049-587 Sequence 587, App
30 507 53.6 507 21 US-09-456-357-31 Sequence 31, Appl1
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38 505.8 53.5 507 101 US-60-465-241-1867 Sequence 1867, Ap
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45 448 47.4 18008 40 US-09-949-016-13231 Sequence 13231, A

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ALIGNMENTS

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RESULT 1
US-09-376-154-1
; Sequence 1, Application US/09376154
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D2
; CURRENT APPLICATION NUMBER: US/09/376.154
; CURRENT FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-376-154-1

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Query Match 100.0%; Score 946; DB 20; Length 946;
Best Local Similarity 100.0%; Pred. No. 2e-200;
Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGGGCTAGGGGCGGGCTGAGATCGGGCTTGAGGCGCCAGAGATGTTCCAG 60

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US-09-922-378-1
; Sequence 1, Application US/09922378
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922.378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15

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SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 946
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-922-378-1

Query Match 100.0%; Score 946; DB 39; Length 946;
 Best Local Similarity 100.0%; Pred. No. 2e-200;
 Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 901 GTACCAATGTTTAATTAAG 946

RESULT 3
 US-10-066-179-1
 Sequence 1, Application US/10066179

GENERAL INFORMATION:
 APPLICANT: Horne, William A.
 APPLICANT: Olerdorf, Tilmann
 TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
 TITLE OF INVENTION: ACIDS AND METHODS OF USE
 FILE REFERENCE: 480140.428C1
 CURRENT APPLICATION NUMBER: US/10/066,179
 CURRENT FILING DATE: 2002-02-01
 NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 946
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-066-179-1

Query Match 100.0%; Score 946; DB 45; Length 946;
 Best Local Similarity 100.0%; Pred. No. 2e-200;
 Matches 946; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 781 CCGTGCCCGCCCTCAGAGTTCCGGGGTTTCCCGAGCGCTCGCTAAGTAGCAGCC 840
Db 781 CCGTGCCCGCCCTCAGAGTTCCGGGGTTTCCCGAGCGCTCGCTAAGTAGCAGCC 840
Qy 841 AGGTTTAAACGTTGTGTACCGGGAGCCGAGCGCCCGGATGCCCTGGGGGCGGTATCA 900
Db 841 AGGTTTAAACGTTGTGTACCGGGAGCCGAGCGCCCGGATGCCCTGGGGGCGGTATCA 900
Qy 901 GTACCAATGTTAATAAAGCCCGCTGTGTGCCAATAAAAAAAAA 946
Db 901 GTACCAATGTTAATAAAGCCCGCTGTGTGCCAATAAAAAAAAA 946

RESULT 4
US-10-209-967-1
; Sequence 1, Application US/10209967
; GENERAL INFORMATION:
; APPLICANT: MUNGER, JOSHUA
; APPLICANT: ROITZMAN, BERNARD
; TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
; FILE REFERENCE: ARCD:380US
; CURRENT APPLICATION NUMBER: US/10/209,967
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 60/308,929
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Human BAD
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(555)
US-10-209-967-1

Query Match 99.9%; Score 945; DB 48; Length 945;
Best Local Similarity 100.0%; Pred. No. 3,4e-200;
Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCTTAGGGGCGCGGCTCAGAGGCGCTTGAGATCGGGCTTGGGCCCAAGCATGTTCCAG 60
Db 1 GGGCTTAGGGGCGCGGCTCAGAGGCGCTTGAGATCGGGCTTGGGCCCAAGCATGTTCCAG 60
Qy 61 ATCCAGAGTTTGAACCGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 ATCCAGAGTTTGAACCGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Qy 121 CCGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 121 CCGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy 181 CTCTGTGGAGAGCCAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 CTCTGTGGAGAGCCAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 241 GCTGGGGGCTGTGGAGATCCGAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GCTGGGGGCTGTGGAGATCCGAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 301 GAAAGAGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 GAAAGAGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 CTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 CTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

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Qy 421 TCCTTTAAGAGGAGACTTCTCCGCCGAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 TCCTTTAAGAGGAGACTTCTCCGCCGAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 AGCTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 AGCTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 TCGGCGCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 TCGGCGCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 601 GGGAGAGATTTGATATATATATATATATATATATATATATATATATATATATATATAT 660
Db 601 GGGAGAGATTTGATATATATATATATATATATATATATATATATATATATATATATAT 660
Qy 661 CCGTGCTGTATCTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 CCGTGCTGTATCTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 ACGGAAGTTGTGTCATCGGAAGTTTGGAGTTTCCGCCACAGCCCGGAAAGTGCT 780
Db 721 ACGGAAGTTGTGTCATCGGAAGTTTGGAGTTTCCGCCACAGCCCGGAAAGTGCT 780
Qy 781 CCGTGCCCGCCCTCAGAGTTCCGGGGTTTCCCGAGCGCTGCGCTAAGTAGCAGAGCC 840
Db 781 CCGTGCCCGCCCTCAGAGTTCCGGGGTTTCCCGAGCGCTGCGCTAAGTAGCAGAGCC 840
Qy 841 AGGTTTAAACGTTGTGTACCGGGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 AGGTTTAAACGTTGTGTACCGGGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 901 GTACCAATGTTAATAAAGCCCGCTGTGTGCCAATAAAAAAAAA 945
Db 901 GTACCAATGTTAATAAAGCCCGCTGTGTGCCAATAAAAAAAAA 945

RESULT 5
US-09-652-916-9142
; Sequence 9142, Application US/09652916
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600,1184-001
; CURRENT APPLICATION NUMBER: US/09/652,916
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,103
; NUMBER OF SEQ ID NOS: 10480
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9142
; LENGTH: 1006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-916-9142

Query Match 92.1%; Score 871.2; DB 28; Length 1006;
Best Local Similarity 97.8%; Pred. No. 9.6e-184;
Matches 915; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

Qy 13 CCGGGTACGGGGGCTCGAGATCGGGGCTTGGGCCAGAGAGATGTTCCAGATCCCAAGATT 72
Db 62 CCGGGTACGGGGGCTCGAGATCGGGGCTTGGGCCAGAGAGATGTTCCAGATCCCAAGATT 121
Qy 73 GAGCGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 132
Db 122 GAGCGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
Qy 133 GGGAGAGGGGCTCTAGGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192
Db 182 GGGAGAGGGGCTCTAGGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241

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US-09-699-997-10996
; Sequence 10996, Application US/09699997
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; APPLICANT: Sliob-Santiago, Immaculada
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2020-001
; CURRENT APPLICATION NUMBER: US/09/699,997
; PRIOR FILING DATE: 2000-10-30
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 12714
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10996
; LENGTH: 1006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-699-997-10996

Query Match      92.1%; Score 871.2; DB 30; Length 1006;
Best Local Similarity 97.8%; Pred. No. 9.6e-184;
Matches 915; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

QY 13 CCGGGTCAGAGGCTTCAGATCGGGCTTGGGCCAGAGCATGTTCCAGATCCAGAGTTT 72
DB 62 CCGGGTCAGAGGCTTCAGATCGGGCTTGGGCCAGAGCATGTTCCAGATCCAGAGTTT 121
QY 73 GAGCCAGTGAAGAGAAAGTCTCAGCTCTGCAAGAGAGGAGGCTGGGCCAGCCCGCA 132
DB 122 GAGCCAGTGAAGAGAAAGTCTCAGCTCTGCAAGAGAGGAGGCTGGGCCAGCCCGCA 181
QY 133 GGGGACGGGCTTCAGGCTCCGGCAAGATGATGCGCAAGGCTCCAGGCTCTGTGGAGC 192
DB 182 GGGGACGGGCTTCAGGCTCCGGCAAGATGATGCGCAAGGCTCCAGGCTCTGTGGAGC 241
QY 193 GCCAGTACACAGAGAGAGAGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
DB 242 GCCAGTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
QY 253 GAGATCCGAGTCCGCAAGTCTCAAGCTCCGCGGGAGAGAGAGAGAGAGAGAGAGAG 312
DB 302 GAGATCCGAGTCCGCAAGTCTCAAGCTCCGCGGGAGAGAGAGAGAGAGAGAGAGAG 361
QY 313 GAGAGAGCCAGCCCTTCGCGGGGCGCTCGGCGCTCGGCGCCCAACCTGTGGAGCA 372
DB 362 GAGAGAGCCAGCCCTTCGCGGGGCGCTCGGCGCTCGGCGCCCAACCTGTGGAGCA 421
QY 373 CAGGCTATGAGCGCGAGAGCTCCGAGAGATGATGATGATGATGATGATGATGATGAT 432
DB 422 CAGGCTATGAGCGCGAGAGCTCCGAGAGATGATGATGATGATGATGATGATGATGAT 481
QY 433 GAGCTTCTGCGCCGAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
DB 482 GAGCTTCTGCGCCGAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541
QY 493 ACGGAGTCTTCAGTCTGAGTGGAGATGGAATTTGGGCAAGGAGAGAGAGAGAGAGAG 552
DB 542 ACGGAGTCTTCAGTCTGAGTGGAGATGGAATTTGGGCAAGGAGAGAGAGAGAGAGAG 601
QY 553 CAGGAGCTTCGAGTCCAGATCCCGAAG-TCCAGCCGTTCCAGTCCGTTGGAGAGAGAG 611
DB 602 CAGGAGCTTCGAGTCCAGATCCCGAAGTCCAGCCGTTCCAGTCCGTTGGAGAGAGAG 661
QY 612 TTGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671
DB 662 TTGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 672 CTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730
DB 721 CTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

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QY 731 GGTCCATCGGAAGTTTGGGTTTCCGCCACAGCCCGCGAAGTGGCTCCGTGGCCCC 790
DB 781 GGTCCATCGGAAGTTTGGGTTTCCGCCACAGCCCGCGAAGTGGCTCCGTGGCCCC 840
QY 791 GCGCTCAGGTTCCGGGTTTCCGCCAGAGGCTTCGCTAAGTGAAGCCAGAGTTTAAC 850
DB 841 GCGCTCAGGTTCCGGGTTTCCGCCAGAGGCTTCGCTAAGTGAAGCCAGAGTTTAAC 900
QY 851 GTTGTGCAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 910
DB 901 GTTGTGCAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 911 TTAATAAGCCCGGTGTGTGCCAAAAA 946
DB 961 TTAATAAGCCCGGTGTGTGCCAAAAA 996

RESULT 8
US-09-726-787-2372
; Sequence 2372, Application US/09726787
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2010-001
; CURRENT APPLICATION NUMBER: US/09/726,787
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 3241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2372
; LENGTH: 1006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-787-2372

Query Match      92.1%; Score 871.2; DB 32; Length 1006;
Best Local Similarity 97.8%; Pred. No. 9.6e-184;
Matches 915; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

QY 13 CCGGGTCAGAGGCTTCAGATCGGGCTTGGGCCAGAGCATGTTCCAGATCCAGAGTTT 72
DB 62 CCGGGTCAGAGGCTTCAGATCGGGCTTGGGCCAGAGCATGTTCCAGATCCAGAGTTT 121
QY 73 GAGCCAGTGAAGAGAAAGTCTCAGCTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 132
DB 122 GAGCCAGTGAAGAGAAAGTCTCAGCTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 181
QY 133 GGGGACGGGCTTCAGGCTCCGGCAAGATGATGCGCAAGGCTCCAGGCTCTGTGGAGC 192
DB 182 GGGGACGGGCTTCAGGCTCCGGCAAGATGATGCGCAAGGCTCCAGGCTCTGTGGAGC 241
QY 193 GCCAGTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
DB 242 GCCAGTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
QY 253 GAGATCCGAGTCCGCAAGTCTCAAGCTCCGCGGGAGAGAGAGAGAGAGAGAGAGAG 312
DB 302 GAGATCCGAGTCCGCAAGTCTCAAGCTCCGCGGGAGAGAGAGAGAGAGAGAGAGAG 361
QY 313 GAGAGAGCCAGCCCTTCGCGGGGCGCTCGGCGCTCGGCGCCCAACCTGTGGAGCA 372
DB 362 GAGAGAGCCAGCCCTTCGCGGGGCGCTCGGCGCTCGGCGCCCAACCTGTGGAGCA 421
QY 373 CAGGCTATGAGCGCGAGAGCTCCGAGAGATGATGATGATGATGATGATGATGATGAT 432
DB 422 CAGGCTATGAGCGCGAGAGCTCCGAGAGATGATGATGATGATGATGATGATGATGAT 481
QY 433 GAGCTTCTGCGCCGAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
DB 482 GAGCTTCTGCGCCGAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541

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QY 493 ACGGAGTCTTCCAGTCTGCTGAGATCGGAATTGGGAGGGAAGCTCCGCCCTCC 552
DB 542 ACGGAGTCTTCCAGTCTGCTGAGATCGGAATTGGGAGGGAAGCTCCGCCCTCC 601
QY 553 CAGTACCTTCCGATCCATCCCGAAA-TCACCCCTTCCATTCCTGGGAGGCAAT 611
DB 602 CAGTACCTTCCGATCCATCCCGAAA-TCACCCCTTCCATTCCTGGGAGGCAAT 661
QY 612 TTGAATATGGGAGGAGTAACTTCCCTCAGGAGGCTATGCAAAAAGAGATCCGTCGTAT 671
DB 662 TTGAATATGGGAGGAGTAACTTCCCTCAGGAGGCTATGCAAAAAGAGATCCGTCGTAT 720
QY 672 CCTTGGAGGAGGAGGTTGACCCAGATTCCTTCCGCTGTGTGAGAACCAAGG-TT 730
DB 721 CCTTGGAGGAGGAGGTTGACCCAGATTCCTTCCGCTGTGTGAGAACCAAGG-TT 780
QY 731 GGTCCATCGGAAGTTTGGGTTTCCGCCACAGCCGCCGGAAGTGGCTCCGTGCCCC 790
DB 781 GGTCCATCGGAAGTTTGGGTTTCCGCCACAGCCGCCGGAAGTGGCTCCGTGCCCC 840
QY 791 GGCCTCAGGTTCCGGGGTTTCCGCCAGGAGGCTGCTGATGAGCAAGTTTAAAC 850
DB 841 GGCCTCAGGTTCCGGGGTTTCCGCCAGGAGGCTGCTGATGAGCAAGTTTAAAC 900
QY 851 GTTGTGTACACCGGAGCCCGAGCCCGGCGATGCTGGGGGCGGTGATCAGTCAAAATG 910
DB 901 GTTGTGTACACCGGAGCCCGAGCCCGGCGATGCTGGGGGCGGTGATCAGTCAAAATG 960
QY 911 TTAATTAAGCCCGCGTGTGTGCCAAAAA 946
DB 961 TTAATTAAGCCCGCGTGTGTGCCAAAAA 996

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RESULT 9
US-09-726-809-2815
; Sequence 2815, Application US/09726809
; GENERAL INFORMATION:
; APPLICANT: Geating, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2011-001
; CURRENT APPLICATION NUMBER: US/09/726,809
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,039
; NUMBER OF SEQ ID NOS: 3268
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2815
; LENGTH: 1006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-809-2815

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Query Match 92.1%; Score 871.2; DB 32; Length 1006;
Best Local Similarity 97.8%; Pred. No. 9.6e-184;
Matches 915; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
QY 13 CCGGTCAGGAGCTTCAGATCGGGCTTGGGCCAGAGATGTTCCAGATCCAGAGTTT 72
DB 62 CCGGTCAGGAGCTTCAGATCGGGCTTGGGCCAGAGATGTTCCAGATCCAGAGTTT 121
QY 73 GAGCCGAGTGAAGAGAAATCTCAGCTTCGAGAGAGGGGCTGGGCCAGGCCCGCA 132
DB 122 GAGCCGAGTGAAGAGAAATCTCAGCTTCGAGAGAGGGGCTGGGCCAGGCCCGCA 181
QY 133 GGGGACGGGCGCTCAGGCTCCGCAAGATCGCAGAGCCCGAGGCTCCGTGGGAGC 192
DB 182 GGGGACGGGCGCTCAGGCTCCGCAAGATCGCAGAGCCCGAGGCTCCGTGGGAGC 241
QY 193 GCGAGTCAACAGAGAGAGCAACAGAGAGGATCATGAGAGGCTGGGGCTGTG 252

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DB 242 GCCAGTCAACAGAGAGAGCCAAACAGACAGGATCATGAGGCGCTGGGCTGTG 301
QY 253 GAGATCCGAGTCCGACAGCTCTAATCCCGGGGGGAGGAGAGAGAGAGAGGAG 312
DB 302 GAGATCCGAGTCCGACAGCTCTAATCCCGGGGGGAGGAGAGAGAGAGAGGAG 361
QY 313 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 372
DB 362 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 421
QY 373 CAGGCTATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 432
DB 422 CAGGCTATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 481
QY 433 GAGCTTCTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492
DB 482 GAGCTTCTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541
QY 493 ACGGAGTCTTCCAGTCTGCTGAGATCGGAATTGGGAGGGAAGCTCCGCCCTCC 552
DB 542 ACGGAGTCTTCCAGTCTGCTGAGATCGGAATTGGGAGGGAAGCTCCGCCCTCC 601
QY 553 CAGTACCTTCCGATCCATCCCGAAA-TCACCCCTTCCATTCCTGGGAGGCAAT 611
DB 602 CAGTACCTTCCGATCCATCCCGAAA-TCACCCCTTCCATTCCTGGGAGGCAAT 661
QY 612 TTGAATATGGGAGGAGTAACTTCCCTCAGGAGGCTATGCAAAAAGAGATCCGTCGTAT 671
DB 662 TTGAATATGGGAGGAGTAACTTCCCTCAGGAGGCTATGCAAAAAGAGATCCGTCGTAT 720
QY 672 CCTTGGAGGAGGAGGTTGACCCAGATTCCTTCCGCTGTGTGAGAACCAAGG-TT 730
DB 721 CCTTGGAGGAGGAGGTTGACCCAGATTCCTTCCGCTGTGTGAGAACCAAGG-TT 780
QY 731 GGTCCATCGGAAGTTTGGGTTTCCGCCACAGCCGCCGGAAGTGGCTCCGTGCCCC 790
DB 781 GGTCCATCGGAAGTTTGGGTTTCCGCCACAGCCGCCGGAAGTGGCTCCGTGCCCC 840
QY 791 GGCCTCAGGTTCCGGGGTTTCCGCCAGGAGGCTGCTGATGAGCAAGTTTAAAC 850
DB 841 GGCCTCAGGTTCCGGGGTTTCCGCCAGGAGGCTGCTGATGAGCAAGTTTAAAC 900
QY 851 GTTGTGTACACCGGAGCCCGAGCCCGGCGATGCTGGGGGCGGTGATCAGTCAAAATG 910
DB 901 GTTGTGTACACCGGAGCCCGAGCCCGGCGATGCTGGGGGCGGTGATCAGTCAAAATG 960
QY 911 TTAATTAAGCCCGCGTGTGTGCCAAAAA 946
DB 961 TTAATTAAGCCCGCGTGTGTGCCAAAAA 996

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RESULT 10
US-09-705-256A-5838
; Sequence 5838, Application US/09705256A
; GENERAL INFORMATION:
; APPLICANT: Ma, Xiao-Jun; Dotsen, Stanton B.; Monsanto Company
; TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, treatme
; FILE REFERENCE: 3214
; CURRENT APPLICATION NUMBER: US/09/705,256A
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: US 60/164,285
; NUMBER OF SEQ ID NOS: 8259
; SEQ ID NO 5838
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-705-256A-5838

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Query Match 91.1%; Score 861.4; DB 31; Length 962;
Best Local Similarity 97.9%; Pred. No. 1.5e-181;
Matches 904; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

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QY 13 CCGGGTCAGGGGCTTCAGATCGGGCTTGGGCCAGACATGTTCCAGATCCAGAGTTT 72
DB 39 CCGGGTCAGGGGCTTCAGATCGGGCTTGGGCCAGACATGTTCCAGATCCAGAGTTT 98
QY 73 GAGCCGAGTGAAGCAAGAAAGACTCCAGCTCTGCAAGAGAGGGCTTGGGCCAGACCCCA 132
DB 99 GAGCCGAGTGAAGCAAGAAAGACTCCAGCTCTGCAAGAGAGGGCTTGGGCCAGACCCCA 158
QY 133 GGGGACGGGGCCCTCAGGCTCCGGCAAGCATATCGCCAGGCCCCAGGCTCTGTGGGAC 192
DB 159 GGGGACGGGGCCCTCAGGCTCCGGCAAGCATATCGCCAGGCCCCAGGCTCTGTGGGAC 218
QY 193 GCCAGTCAACAGAGAGAGAGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
DB 219 GCCAGTCAACAGAGAGAGAGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 278
QY 253 GAGATCCGAGAGTCCGCAAGCTCTTACCCCGGGGAGAGAGAGAGAGAGAGAGAGAGAG 312
DB 279 GAGATCCGAGAGTCCGCAAGCTCTTACCCCGGGGAGAGAGAGAGAGAGAGAGAGAGAG 338
QY 313 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
DB 339 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 398
QY 373 CAGGCTATGAGCCGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
DB 399 CAGGCTATGAGCCGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 458
QY 433 GAGATCTCTCCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
DB 459 GAGATCTCTCCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 518
QY 493 ACGGAGTCTTCAGTCCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
DB 519 ACGGAGTCTTCAGTCCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
QY 553 CAGTGACCTTCGAGTCCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 611
DB 579 CAGTGACCTTCGAGTCCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 638
QY 612 TTGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671
DB 639 TTGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 697
QY 672 CCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730
DB 698 CCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 757
QY 731 GGTCCCATCGAAGATTTTGGGTTTCCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
DB 758 GGTCCCATCGAAGATTTTGGGTTTCCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 817
QY 791 GGTCCCATCGAAGATTTTGGGTTTCCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850
DB 818 GGTCCCATCGAAGATTTTGGGTTTCCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 877
QY 851 GTTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 910
DB 878 GTTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 937
QY 911 TTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 933
DB 938 TTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

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RESULT 11
US-60-164-285-5838
: Sequence 5838, Application us/60164285.
: GENERAL INFORMATION:
: APPLICANT: Ma, Xiao-Jun
: TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, treatme
: FILE REFERENCE: 3214

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: CURRENT APPLICATION NUMBER: US/60/164,285
: CURRENT FILING DATE: 1999-11-05
: NUMBER OF SEQ ID NOS: 8259
: SEQ ID NO 5838
: LENGTH: 962
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-164-285-5838

Query Match      91.1%; Score 861.4; DB 70; Length 962;
Best Local Similarity 97.9%; Pred. No. 1.5e-181;
Matches 904; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

QY 13 CCGGGTCAGGGGCTTCAGATCGGGCTTGGGCCAGACATGTTCCAGATCCAGAGTTT 72
DB 39 CCGGGTCAGGGGCTTCAGATCGGGCTTGGGCCAGACATGTTCCAGATCCAGAGTTT 98
QY 73 GAGCCGAGTGAAGCAAGAAAGACTCCAGCTCTGCAAGAGAGGGCTTGGGCCAGACCCCA 132
DB 99 GAGCCGAGTGAAGCAAGAAAGACTCCAGCTCTGCAAGAGAGGGCTTGGGCCAGACCCCA 158
QY 133 GGGGACGGGGCCCTCAGGCTCCGGCAAGCATATCGCCAGGCCCCAGGCTCTGTGGGAC 192
DB 159 GGGGACGGGGCCCTCAGGCTCCGGCAAGCATATCGCCAGGCCCCAGGCTCTGTGGGAC 218
QY 193 GCCAGTCAACAGAGAGAGAGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
DB 219 GCCAGTCAACAGAGAGAGAGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 278
QY 253 GAGATCCGAGAGTCCGCAAGCTCTTACCCCGGGGAGAGAGAGAGAGAGAGAGAGAGAG 312
DB 279 GAGATCCGAGAGTCCGCAAGCTCTTACCCCGGGGAGAGAGAGAGAGAGAGAGAGAGAG 338
QY 313 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
DB 339 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 398
QY 373 CAGGCTATGAGCCGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
DB 399 CAGGCTATGAGCCGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 458
QY 433 GAGATCTCTCCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
DB 459 GAGATCTCTCCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 518
QY 493 ACGGAGTCTTCAGTCCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
DB 519 ACGGAGTCTTCAGTCCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
QY 553 CAGTGACCTTCGAGTCCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 611
DB 579 CAGTGACCTTCGAGTCCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 638
QY 612 TTGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671
DB 639 TTGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 697
QY 672 CCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730
DB 698 CCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 757
QY 731 GGTCCCATCGAAGATTTTGGGTTTCCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
DB 758 GGTCCCATCGAAGATTTTGGGTTTCCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 817
QY 791 GGTCCCATCGAAGATTTTGGGTTTCCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850
DB 818 GGTCCCATCGAAGATTTTGGGTTTCCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 877
QY 851 GTTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 910
DB 878 GTTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 937

```

QY 911 TTAATAAGCCCGCTGTGTGCC 933
DB 938 TTAATAAGCCCGCTGTGTGCC 960

RESULT 12

US-09-894-657-2
Sequence 2, Application US/09894657
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.

Yue, Henry
Lai, Preeti
Shah, Puri
Corley, Neil C.

TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657

FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-4166

TELEFAX: 650-855-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 1105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: 358673

CLONE: SYNORAB01
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-894-657-2

Query Match 88.8%; Score 840.4; DB 37; Length 1105;
Best Local Similarity 97.9%; Pred. No. 7,1e-177;
Matches 883; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

QY 43 GCCCAGAGCATGTTCCAGATCCCAAGTTTGAAGCCAGAGTGAAGAGAGTCCAGCTCT 102
DB 205 GCCCAGAGCATGTTCCAGATCCCAAGTTTGAAGCCAGAGTGAAGAGAGTCCAGCTCT 264
QY 103 GGAGAGAGGGGCTGGGCCCCCAGCCCCGAGAGGAGAGGGGCTTCAGGCTCCGGCAAGCT 162
DB 265 GGAGAGAGGGGCTGGGCCCCCAGCCCCGAGAGGAGAGGGGCTTCAGGCTCCGGCAAGCT 324
QY 163 CATCCGACAGGCCCCCAGGCTCTCTGTGGAGCGCCAGTCAACAGAGAGAGCAACAGC 222
DB 325 CATCCGACAGGCCCCCAGGCTCTCTGTGGAGCGCCAGTCAACAGAGAGAGCAACAGC 384
QY 223 AGCAGCCATCATGAGAGCGCTGGGGCTGTGAGAGATCCGAGTGCACAGCTCTTACCCC 282
DB 385 AGCAGCCATCATGAGAGCGCTGGGGCTGTGAGAGATCCGAGTGCACAGCTCTTACCCC 444

QY 283 GCGGGAGCGAG 342
DB 445 GCGGGAGCGAG 504
QY 343 CGCTGGGCGCCCCCAACCTCTGGGACAGACAGGCTATAGCGGAGCTCCGAGAGATG 402
DB 505 CGCTGGGCGCCCCCAACCTCTGGGACAGACAGGCTATAGCGGAGCTCCGAGAGATG 564
QY 403 AGTGAAGATTGTGTGACTCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
DB 565 AGTGAAGATTGTGTGACTCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 624
QY 463 GCAAGCAGATGCGGCAAGCTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
DB 625 GCAAGCAGATGCGGCAAGCTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 684
QY 523 AACTTGGGCGAGGAG 581
DB 685 AACTTGGGCGAGGAG 744
QY 582 CACCGCTTCCCATTTGCTGGGACAGCATTTTGAATATGAGAGAGAGAGAGAGAGAGAG 641
DB 745 CACCGCTTCCCATTTGCTGGGACAGCATTTTGAATATGAGAGAGAGAGAGAGAGAGAG 803
QY 642 GCTATGCAAAAAG 701
DB 804 GCTATGCAAAAAG 863
QY 702 TTCCGGTGTGTGTAAGCAG 760
DB 864 TTCCGGTGTGTGTAAGCAG 923
QY 761 CACAGCCGCGGAG 820
DB 924 CACAGCCGCGGAG 983
QY 821 CCTGCGTAAAGTGAAG 880
DB 984 CCTGCGTAAAGTGAAG 1043
QY 881 TGCCCTGGGGGCGGTGATCAGTACCAATGTTAATAAAGCCGCGTGTGTGCAAAAAA 940
DB 1044 TGCCCTGGGGGCGGTGATCAGTACCAATGTTAATAAAGCCGCGTGTGTGCAAAAAA 1103
QY 941 AA 942
DB 1104 AA 1105

RESULT 13

US-60-172-373-13906
Sequence 13906, Application US/60172373
GENERAL INFORMATION:

APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh

TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
FILE REFERENCE: GX-0006 P
CURRENT APPLICATION NUMBER: US/60/172,373

CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 25,772

SOFTWARE: PERL Program
SEQ ID NO 13906
LENGTH: 1143

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 196568.3
US-60-172-373-13906


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Db      960 CACAGCCGCGGAGGCTCCGTCGCCCCGCCCTCAGGCTCCGGCTTTCCCCAGGGG 1019
QY      821 CCTGCGCTAAGTAGAGCCAGGCTTTAACTGTTGTCAACGGGACCCGAGCCCGCGCA 880
Db      1020 CTTGCGCTAAGTAGAGCCAGGCTTTAACTGTTGTCAACGGGACCCGAGCCCGCGCA 1079
QY      881 TGCCCTGGGGGCGGTGATCAGTACCAATGTTAATAAAGCCCGGTGTGTCCAAAMAAA 940
Db      1080 TGCCCTGGGGGCGGTGATCAGTACCAATGTTAATAAAGCCCGGTGTGTGTCCAAAMAAA 1139
QY      941 AAAA 944
Db      1140 AAAA 1143

RESULT 15
PCT-US03-07713-369
Sequence 369, Application PC/TUS0307713
GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH
APPLICANT: Baker, Joffe B.
APPLICANT: Cronin, Maureen T.
APPLICANT: Kiefer, Michael C.
APPLICANT: Shak, Steve
APPLICANT: Walker, Michael Graham
TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
FILE REFERENCE: 39740-0001.PCT
CURRENT APPLICATION NUMBER: PCT/US03/07713
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/412,049
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/364,890
PRIOR FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 384
SOFTWARE: fastSeq for Windows Version 4.0
SEQ ID NO 369
LENGTH: 1127
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US03-07713-369

Query Match      88.1%; Score 833; DB 1; Length 1127;
Best Local Similarity 98.0%; Pred. No. 3, 2e-175;
Matches 875; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

QY      43 GCCCAGAGCATTTCCAGATCCCAAGTTTGAAGCCGAGTGAAGAGAGTCTCCAGCTCT 102
Db      233 GCCCAGAGCATTTCCAGATCCCAAGTTTGAAGCCGAGTGAAGAGAGTCTCCAGCTCT 292
QY      103 GCAGAGAGGGGCTGGGCGCCGAGCCCGCAGGGGAGCGGGCCCTCAAGGCTCCGGCAAGCAT 162
Db      293 GCAGAGAGGGGCTGGGCGCCGAGCCCGCAGGGGAGCGGGCCCTCAAGGCTCCGGCAAGCAT 352
QY      163 CATGCCAGAGCCCGAGGCTCTCTGTGGAGCGCCAGTCAACAGCAGAGAGAGCCCAACAGC 222
Db      353 CATGCCAGAGCCCGAGGCTCTCTGTGGAGCGCCAGTCAACAGCAGAGAGAGCCCAACAGC 412
QY      223 AGCAGCCATCATGAGGCGCTGGGGCTGTGAGATCCGGAGTCCGACAGCTCTTAACCC 282
Db      413 AGCAGCCATCATGAGGCGCTGGGGCTGTGAGATCCGGAGTCCGACAGCTCTTAACCC 472
QY      283 GCGGGGAGCGAGAGAGAGAGATGGGGGAGAGCCCAAGCCCTTTCCGGGGCGGCTCG 342
Db      473 GCGGGGAGCGAGAGAGAGAGATGGGGGAGAGCCCAAGCCCTTTCCGGGGCGGCTCG 532
QY      343 GCGTGGGCGCCCAACCTCTGGGAGAGCAGCAGCTATGCGCGAGCTCCGAGAGATG 402
Db      533 GCGTGGGCGCCCAACCTCTGGGAGAGCAGCAGCTATGCGCGAGCTCCGAGAGATG 592
QY      403 AGTGAAGATTGTGAGCTCTTTAAAGAGGACTTCTCGCCGAGAGAGCGGGCACA 462
Db      593 AGTGAAGATTGTGAGCTCTTTAAAGAGGACTTCTCGCCGAGAGAGCGGGCACA 652

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QY      463 GCAGCAGATGCGGCAAGCTCCAGCTGACGCGAGTCTTCAAGTCCGTGTGGATCG 522
Db      653 GCAGCAGATGCGGCAAGCTCCAGCTGACGCGAGTCTTCAAGTCCGTGTGGATCG 712
QY      523 AACTTGGGAGGAGAGTCCGCCCCCTCCAGTGAATCTTGGGTCAATCCGAAA-TC 581
Db      713 AACTTGGGAGGAGAGTCCGCCCCCTCCAGTGAATCTTGGGTCAATCCGAAA-TC 772
QY      582 CACCCGTTCCATGCCCCGCGGAGCCATTTGAATAGGAGAGATGATTCCTCAG 641
Db      773 CACCCGTTCCATGCCCCGCGGAGCCATTTGAATAGGAGAGATGATTCCTCAG 831
QY      642 GCTATGCAAAAAGAGATCCGTGCTATCTTTGAGAGAGGTTGACCAATTC 701
Db      832 GCTATGCAAAAAGAGATCCGTGCTATCTTTGAGAGAGGTTGACCAATTC 891
QY      702 TTCGGGTGTGTGAAGCCAGGAAAG-TTGATCCATCGAAGTTTGGTTTCCGCC 760
Db      892 TTCGGGTGTGTGAAGCCAGGAAAGCTTGATCCATCGAAGTTTGGTTTCCGCC 951
QY      761 CACAGCCGCGGAAGTGGCTCGTGGCCCGCCCTCAGGTTCCGGGGTTTCCCGAGGCG 820
Db      952 CACAGCCGCGGAAGTGGCTCGTGGCCCGCCCTCAGGTTCCGGGGTTTCCCGAGGCG 1011
QY      821 CCTGGCTAAGTAGAGCCAGGTTTAACTGTTGTCAACGGGAGCCGAGCCCGCGCA 880
Db      1012 CCTGGCTAAGTAGAGCCAGGTTTAACTGTTGTCAACGGGAGCCGAGCCCGCGCA 1071
QY      881 TGCCCTGGGGGCGGTGATCACTACCAAAATGTTAATAAAGCCCGGTGTGCC 933
Db      1072 TGCCCTGGGGGCGGTGATCACTACCAAAATGTTAATAAAGCCCGGTGTGCC 1124

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Job time : 19251 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 15:18:18 / Search time 1645 Seconds
(without alignments)
1359.187 Million cell updates/sec

Title: US-10-066-179-1

Perfect score: 946
Sequence: 1 g99cctagggcgccggtca.....gtctgcaaaaaaaaaa 946

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4472476 seqs, 1181745796 residues

Total number of hits satisfying chosen parameters: 8944952

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861.4	91.1	956	US-60-490-890-170	Sequence 170, App
2	833	88.1	1127	US-60-490-890-168	Sequence 168, App
3	505.8	53.5	507	US-60-487-610-625	Sequence 625, App
4	447.6	47.3	26007	US-60-487-610-19554	Sequence 19554, A
5	200.6	21.2	201	US-60-487-610-9557	Sequence 9557, App
6	194	20.5	293	US-09-540-233D-92408	Sequence 92408, A
7	190.8	20.2	564	US-60-487-610-49731	Sequence 49731, A
8	167.8	17.7	501	US-60-507-481-6599	Sequence 6599, App
9	160.4	17.0	201	US-60-487-610-49732	Sequence 49732, A
10	155.6	16.4	156	US-60-487-610-9558	Sequence 9558, App
11	126.6	13.4	201	US-60-487-610-49733	Sequence 49733, A
12	117.6	12.4	118	US-60-487-610-9559	Sequence 9559, App
13	48.2	5.1	100	US-10-664-025-13836	Sequence 13836, A
14	47.6	5.0	80	US-10-384-245-499	Sequence 499, App
15	42.2	4.5	2182	PCT-US03-10720-69	Sequence 69, App
16	41.2	4.4	2194	US-10-723-860-678	Sequence 678, App
17	41.2	4.4	3430	US-60-500-337-980	Sequence 980, App
18	41.2	4.4	4232	US-60-500-337-981	Sequence 981, App
19	41.2	4.4	4247	US-60-500-337-981	Sequence 981, App
20	41.2	4.4	4399	PCT-US03-28227-1095	Sequence 1095, App
21	41.2	4.4	4694	US-10-723-860-5310	Sequence 5310, App
22	41.2	4.4	28905	US-60-500-337-19324	Sequence 19324, A
23	41.2	4.4	208820	US-60-495-114-16936	Sequence 16936, A
24	40	4.2	32329	US-10-374-903A-1	Sequence 1, Appl1
25	40	4.2	39657	US-60-495-114-16564	Sequence 16564, A

C 26	39.8	4.2	99538	8	US-60-487-610-19760	Sequence 19760, A
C 27	39.4	4.2	364	6	US-10-664-025-17202	Sequence 17202, A
C 28	39.4	4.2	3914	6	US-10-723-860-6677	Sequence 6677, App
C 29	39	4.1	2126	6	US-10-723-860-3054	Sequence 3054, App
C 30	39	4.1	2361	6	US-10-723-860-7081	Sequence 7081, App
C 31	39	4.1	79669	8	US-60-495-114-16657	Sequence 16657, A
C 32	39	4.1	85692	1	US-60-499-964-5178	Sequence 5178, App
C 33	39	4.1	85692	1	PCT-US03-18787-1	Sequence 1, Appl1
C 34	39	4.1	85692	1	PCT-US03-19069-1	Sequence 1, Appl1
C 35	38.8	4.1	2898	7	US-10-701-283-5	Sequence 5, Appl1
C 36	38.8	4.1	2916	7	US-10-701-283-5	Sequence 5, Appl1
C 37	38.8	4.1	3132	7	US-10-476-191-56	Sequence 56, Appl1
C 38	38.8	4.1	3132	7	US-10-701-283-7	Sequence 7, Appl1
C 39	38.6	4.1	505	6	US-10-664-025-15639	Sequence 15639, A
C 40	38.6	4.1	122496	8	US-60-487-610-19283	Sequence 19283, A
C 41	38.6	4.1	122496	8	US-60-485-450-11884	Sequence 11884, A
C 42	38.4	4.1	2406	7	US-10-472-987-1	Sequence 1, Appl1
C 43	38.4	4.1	18895	8	US-60-524-882-9233	Sequence 9233, App
C 44	38.4	4.1	127508	7	US-10-322-281-158	Sequence 158, App
C 45	38.4	4.1	258386	8	US-60-500-337-19783	Sequence 19783, A

ALIGNMENTS

RESULT 1									
US-60-490-890-170									
Sequence 170, Application US/60490890									
GENERAL INFORMATION:									
APPLICANT: Li, Martha									
APPLICANT: Rupnow, Brent A.									
APPLICANT: Webster, Kevin R.									
APPLICANT: Jackson, Donald									
APPLICANT: Wong, Tai W.									
TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION									
FILE REFERENCE: D0310 PSP									
CURRENT APPLICATION NUMBER: US/60/490,890									
CURRENT FILING DATE: 2003-07-29									
NUMBER OF SEQ ID NOS: 2779									
SOFTWARE: PatentIn version 3.2									
SEQ ID NO 170									
LENGTH: 956									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-60-490-890-170									
Query Match									
Best Local Similarity 97.9%; Pred. No. 3.3e-208;									
Matches 904; Conservative 0; Mismatches 16; Indels 3; Gaps 3;									
QY	13	CGGGTCAGGGGCTTCGAGATCGGGCTTGGGCCCCAGACATGTTCCAGATCCAGAGTTT	72						
DB	32	CGGGTCAGGGTCTTCGAGATCGGGCTTGGGCCCAAGCATGTTCCAGATCCAGAGTTT	91						
QY	73	GAGCCGATGAGCAGGAGAGACTTCAGCTCTGACAGAGAGGGGCTTGGGCCCCAGCCCGCA	132						
DB	92	GAGCCGATGAGCAGGAGAGACTTCAGCTCTGACAGAGAGGGGCTTGGGCCCCAGCCCGCA	151						
QY	133	GGGGAACGGGCGCTTCAGGCTTCGGCAAGCATCATCGCCAGGCCCTCTGTGTGGAGC	192						
DB	152	GGGGAACGGGCGCTTCAGGCTTCGGCAAGCATCATCGCCAGGCCCTCTGTGTGGAGC	211						
QY	193	GCACGTCACACGAGAGAGAGCAACACACAGACAGCATCATGAGAGGCGCTGGGGCTGTG	252						
DB	212	GCACGTCACACGAGAGAGAGCAACACACAGACAGCATCATGAGAGGCGCTGGGGCTGTG	271						
QY	253	GAGATCCGAGTTCGCCACAGCTCTCAACCCCGGGGAGCGAGAGAGAGAGAGATGGGG	312						
DB	272	GAGATCCGAGTTCGCCACAGCTCTCAACCCCGGGGAGCGAGAGAGAGAGATGGGG	331						
QY	313	GAGGAGCCAGGCCCTTTTCGGGGCGGCTTCGGGCGGCTTCGGGCGGCTTCGGGCGGCA	372						
DB	332	GAGGAGCCAGGCCCTTTTCGGGGCGGCTTCGGGCGGCTTCGGGCGGCTTCGGGCGGCA	391						

QY 373 CAGCGCTATGGCCGCGAGCTCCGAGATGATGACGAGTTTGTGACTCTCTTTAAGAG 432
 Db 392 CAGCGCTATGGCCGCGAGCTCCGAGATGATGACGAGTTTGTGACTCTCTTTAAGAG 451
 QY 433 GGACTTCTCCGCGGAGAGCGCGGCAACAGCAACGATCGGCAAAAGTCCAGCTGG 492
 Db 452 GGACTTCTCCGCGGAGAGCGCGGCAACAGCAACGATCGGCAAAAGTCCAGCTGG 511
 QY 493 ACGGAGCTTCCGATCTCGATGGGATGGAACCTTGGGCAAGGAGTCCGCCCTCC 552
 Db 512 ACGGAGCTTCCGATCTCGATGGGATGGAACCTTGGGCAAGGAGTCCGCCCTCC 571
 QY 553 CAGTGAACCTTCCGATCTCCAGTCCGCAAA-TCCACCCGTTCCATTCCTCGGAGCAGCT 611
 Db 572 CAGTGAACCTTCCGATCTCCAGTCCGCAAA-TCCACCCGTTCCATTCCTCGGAGCAGCT 631
 QY 612 TTGAATATGGAGAGAGTGAAGTCTCAGGCTATGCAAAAGAGATCCGTCTGTAT 671
 Db 632 TTGAATATGGAGAGAGTGAAGTCTCAGGCTATGCAAAAGAGATCCGTCTGTAT 690
 QY 672 CCTTGGAGGAGAGGTTGATCCAGATTCCTTCCGATGATGATGAGGCAAGAGG-TT 730
 Db 691 CCTTGGAGGAGAGGTTGATCCAGATTCCTTCCGATGATGATGAGGCAAGAGG-TT 750
 QY 731 GATCCATCGAGAGTGTGGTTTCCGCGCAAGCCGCGAAAGTGGCTCCGTGGCCG 790
 Db 751 GATCCATCGAGAGTGTGGTTTCCGCGCAAGCCGCGAAAGTGGCTCCGTGGCCG 810
 QY 791 GATCCATCGAGAGTGTGGTTTCCGCGCAAGCCGCGAAAGTGGCTCCGTGGCCG 850
 Db 811 GATCCATCGAGAGTGTGGTTTCCGCGCAAGCCGCGAAAGTGGCTCCGTGGCCG 870
 QY 851 GTTGATGATCGGAGAGCCGAGAGCCCGGAGATGCTTGGGCGCGGATCAGTCAAAATG 910
 Db 871 GTTGATGATCGGAGAGCCGAGAGCCCGGAGATGCTTGGGCGCGGATCAGTCAAAATG 930
 QY 911 TTAATTAAGCCCGCGCTGTGTCC 933
 Db 931 TTAATTAAGCCCGCGCTGTGTCC 953

RESULT 2
 US-60-490-890-168
 ; Sequence 168, Application US/60490890
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Martha
 ; APPLICANT: Rupnow, Brent A.
 ; APPLICANT: Webster, Kevin R.
 ; APPLICANT: Jackson, Donald
 ; APPLICANT: Mong, Tai W.
 ; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
 ; FILE REFERENCE: D0310 PSP
 ; CURRENT APPLICATION NUMBER: US/60/490,890
 ; CURRENT FILING DATE: 2003-07-29
 ; NUMBER OF SEQ ID NOS: 2779
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 168
 ; LENGTH: 1127
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-60-490-890-168

Query Match 88.1%; Score 833; DB 8; Length 1127;
 Best Local Similarity 98.0%; Pred. No. 5,4e-201;
 Matches 875; Conservative 0; Mismatches 15; Indels 3; Gaps 3;
 QY 43 GCCGAGCATGTTCCAGATCCAGAGTTTGAAGCGAGTGAAGAGAGTCCAGCTCT 102
 Db 233 GCCGAGCATGTTCCAGATCCAGAGTTTGAAGCGAGTGAAGAGAGTCCAGCTCT 292
 QY 103 GCAGAGAGGAGCTTGGGCGCCAGAGCCGCGAGGAGAGCGGCGCTCAGAGCTCCGAGCAT 162

Db 293 GCAGAGAGGAGCTTGGGCGCCAGAGCCCGAGGAGAGCGGCGCTCAGAGCTCCGAGCAT 352
 QY 163 CATGCGAGGAGCCCGAGGCTCTGTGGGAGAGCCAGTCAAGAGAGAGAGCCAAACGAGC 222
 Db 353 CATGCGAGGAGCCCGAGGCTCTGTGGGAGAGCCAGTCAAGAGAGAGAGCCAAACGAGC 412
 QY 223 AGCAGCATATGAGAGGCGGTGGGCTGTGAGATCCGAGTCCGCAAGCTCTTACCCC 282
 Db 413 AGCAGCATATGAGAGGCGGTGGGCTGTGAGATCCGAGTCCGCAAGCTCTTACCCC 472
 QY 283 GCGGAGAGCGAGAGAGAGAGAGATGAGGAGAGAGAGCCGAGCCCTTTCCGGGCGCGTCC 342
 Db 473 GCGGAGAGCGAGAGAGAGAGATGAGGAGAGAGAGAGCCGAGCCCTTTCCGGGCGCGTCC 532
 QY 343 CGCTCGAGGAGCCCGCAACCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 402
 Db 533 CGCTCGAGGAGCCCGCAACCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 592
 QY 403 AGTGAAGATTTGTGACTCTCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
 Db 593 AGTGAAGATTTGTGACTCTCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 652
 QY 463 GCAACGAGATGAGGAG 522
 Db 653 GCAACGAGATGAGGAG 712
 QY 523 AACTTGGAGAGGAG 581
 Db 713 AACTTGGAGAGGAG 772
 QY 582 CACCGGTTCCATTTGCTCCGAG 641
 Db 773 CACCGGTTCCATTTGCTCCGAG 831
 QY 642 GCTATGCAAAAG 701
 Db 832 GCTATGCAAAAG 891
 QY 702 TTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 760
 Db 892 TTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951
 QY 892 TTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951
 Db 761 CACAGCGCGGAG 820
 Db 952 CACAGCGCGGAG 1011
 QY 821 CTTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 880
 Db 1012 CTTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1071
 QY 881 TGCCCTGGGAGCGGTGATCAGTCAAGTCAATGTTAATAAGCCCGGCGGTGTGTCC 933
 Db 1072 TGCCCTGGGAGCGGTGATCAGTCAAGTCAATGTTAATAAGCCCGGCGGTGTGTCC 1124

RESULT 3
 US-60-487-610-625
 ; Sequence 625, Application US/60487610
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: HUANG, Hongjin
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
 ; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001469
 ; CURRENT APPLICATION NUMBER: US/60/487,610
 ; CURRENT FILING DATE: 2003-07-17
 ; NUMBER OF SEQ ID NOS: 97101
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 625
 ; LENGTH: 507
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-60-487-610-625

Query Match	53.5%	Score 505.8;	DB 8;	Length 507;
Best Local Similarity	99.4%	Pred. No. 3e-118;		
Matches 504; Conservative	3;	Mismatches 0;	Indels 0;	Gaps 0

Qy	52	ATGTTCCAGATCCCAAGATTGAGCCGAAATGAGCAAGAACTCAGCTTCGACGAAG	111
Db	1	ATGTTCCAGATCCCAARTTTGAAGCGAATGACGAAGAACTCAGCTTCGACGAAG	60
Qy	112	GGCCTGGGCCCCAGCCCCGCGAGGGGACGGGCCCCTAGGCTCCGCGACATCATGCCAG	171
Db	61	GGCCTGGGCCCCAGCCCCGCGAGGGGACGGGCCCCTAGGCTCCGCGACATCATGCCAG	120
Qy	172	GCCCCAGGCTCCTGTGGGACGCGAGTACACAGACAGAGACGCCAACAGCAGAGGCAT	231
Db	121	GCCCCAGGCTCCTGTGGGACGCGCACTACACAGACAGAGACGCCAACAGCAGAGGCAT	180
Qy	232	CATGAGGCGCTTGGGCTGTGGAGATCCGAGTGCACACAGCTCTTACCCTCCGCGGGACG	291
Db	181	CATGAGGCGCTTGGGCTGTGGAGATCCGAGTGCACACAGCTCTTACCCTCCGCGGGACG	240
Qy	292	GATGAGAGCGAAGGATGGGGGAGAGGCCACGCCCTTCGGGGCCGCTCGGCTCGGCG	351
Db	241	GATGAGAGCGAAGGATGGGGGAGAGGCCACGCCCTTCGGGGCCGCTCGGCTCGGCG	300
Qy	352	CCCCCAACTCTGGGACAGCAGCGCTATGGCCGCGAGCTCCGAGGATGATGACGAG	411
Db	301	CCCCCAACTCTGGGACAGCAGCGCTATGGCCGCGAGCTCCGAGGATGATGACGAG	360
Qy	412	TTTGTGACTCCTTTAAGAAAGGACTTCCTCGCCCGGAAGACGCGGGACACAGCAACGAG	471
Db	361	TTTGTGACTCCTTTAAGAAAGGACTTCCTCGCCCGGAAGACGCGGGACACAGCAACGAG	420
Qy	472	ATGCGCAAGCTCCAGCTGACGCGAGTCTTCCAGTCTTGATGGATTCGAACTTTGGGC	531
Db	421	ATGCGCAAGCTCCAGCTGACGCGAGTCTTCCAGTCTTGATGGATTCGAACTTTGGGC	480
Qy	532	AGGGGAAGCTCCGCCCCCTCCCAAGTGA	558
Db	481	AGGGGAAGCTCCGCCCCCTCCCAAGTGA	507

RESULT 4
US-60-487-610-19554

[illegible]

Db	19936	GCCTGAGCGGAGGCTCTCAAGTCTCTGTTGGGATTCGAACTTTGGGACAGGGGAAAGCTCCGCC	19999
Qy	548	CTTCCGAGTGACCTTGGTCCACATCCGAAA-TCACCCGTTTCCCATTTGCCCTTGAGCAG	606
Db	19996	CTCTCCAGTGACCTTGGTCTCCACATCTCCGAAACTCCACCCGTTTCCACAGCCCTTGAGCAG	20055
Qy	607	CCATTTTGAATATACGGAAGGAAAGCAATATCTTCAGAGCCATATCCAAAAGGATATCCCTAC	666

QY	607	CCATTTTGAATATAGGAGAGAAAGTAATTCCTCCAGGCTCATATGCAAAAAGAGATCCGTGC	666
Db	20056	CCATCTGAATATATAGGCGGAGAGT-ACTTCCCTCAGGCTATGCAAAAAGAGATCCGTGC	20114
QY	667	TGATCTCTTGGAGGAGGGTTGACCCCAATTCCTTCGGTGTGTGTAACCAAGAA	726
Db	20115	TGCTCTCTTGGAGGAGGGCTGACCCCAATTCCTTCGGTGTGTGTAACCAAGAA	20174
QY	727	GG-TTGATCCCATCGAGATTTTGGGTTTTCGCGCCACAGCGCGGAAGTGGCTCCGTG	785
Db	20175	GGCTTGATCCCATCGAGATTTTGGGTTTTCGCGCCACAGCGCGGAAGTGGCTCCGTG	20234
QY	786	GCCCCGCGCCTCAGGTTCCGGGGTTTCCCGCAGCGCTGTGCGTAAGTAGCGACAGATT	845
Db	20235	GCCCCGCGCCTCAGGCTCCGGGGTTTCCCGCAGCGCTGTGCGTAAGTAGCGACAGATT	20294
QY	846	TAACTGTGTGTACACCGGAGACCCGAGACCCCGCGATGCCCTTGGGGGCGGTATCAGTACC	905
Db	20295	TAACTGTGTGTACACCGGAGACCCGAGACCCCGCGATGCCCTTGGGGGCGGTATCAGTACC	20354
QY	906	AAATGTTAATAAAGCCCGCGGTGTGTCC	933
Db	20355	AAATGTTAATAAAGCCCGCGGTGTGTCC	20382

```

RESULT 5
US-60-487-610-9557
: Sequence 9557, Application US/60487610
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS
: TITLE OF INVENTION: LIVER FIBROSIS IN HE
: TITLE OF INVENTION: METHODS OF DETECTION
: FILE REFERENCE: C0001469
: CURRENT APPLICATION NUMBER: US/60/487, 610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9557
: LENGTH: 201
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-487-610-9557

```

Query Match	21.2%	Score 200.6	DB 8	Length 201
Best Local Similarity	99.5%	Pred. No. 4.3e-41		
Matches 200	Conservative 1	Mismatches 0	Indels 0	Gaps 0
QY	239	GGCGTGGGGCTGTGAGATCCGAGTCCGACACAGCTCTTACCCCGCGGGACGGAGACG	298	
Db	1	GGCGTGGGGCTGTGAGATCCGAGTCCGACACAGCTCTTACCCCGCGGGACGGAGACG	60	
QY	299	ACGAAGGGAATGGGGGAGGAGGCCGCCCCCTTTGGGGGCGCTGCGCTCGGGCCCCCA	358	
Db	61	ACGAAGGGAATGGGGGAGGAGGCCGCCCCCTTTGGGGGCGCTGCGCTCGGGCCCCCA	120	
QY	359	ACCTCTGGGACAGCAGCGCTATGCGCGGAGCTCCGAGGATGAGTGAAGATTGTGTG	418	
Db	121	ACCTCTGGGACAGCAGCGCTATGCGCGGAGCTCCGAGGATGAGTGAAGATTGTGTG	180	
QY	419	ACTCCCTTTAAGAGGGAATTC	439	
Db	181	ACTCCCTTTAAGAGGGAATTC	201	

RESULT 6


```

QY 669 TATCTTTGAGGAGG-----CTTACCACGATTCCTTCGGGTGTGTGAAGCC 720
DB 250 TTCTCTTCGAGAGGAGGCGCATCTGACCCAAAGCCGATCCCTTCGGGTGTGAAGCC 309
QY 721 ACGGAGG---TTGGTCCATCGGAAGTTTG--GGTTTCCGGCCACAGCCCGCGGAG 775
DB 310 CACGAGAGGAGGTTTGGCCCTCGGAGGTTTGAAGTTTACGGCCCTTGGCGCGGAG 369
QY 776 TGGCTCCGTGGCCCGCCCTCAGGTTTC--CGGGGTTTCCCCCAGGCGCTGCGCTAAGTAG 834
DB 370 TGGCCCGGAGCCCGCCCGCCCGCCCGCGCGCTGCGCGCTGCGCGCAAGTAG 429
QY 835 CGAGCCAGGTTTAACTGTTGTGTGACCGGAGCCGAGCCCGCGGAGCTTGGGCGCG 894
DB 430 CGGGCGAGGAGAAACCTTAATCTTCAGAGAGCCCTTCTCCGCGGCGTGTGCGGCGTG 489
QY 895 TGATCAGTACCAA---TCTTAATAAGCCCGCTGTGTGCAAAAAA 946
DB 490 TCACTCGCAACGAATGTGTATATAAGCCCGGTTTGTGCAAAAAA 544

```

RESULT 9

```

US-60-487-610-49732
; Sequence 49732, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49732
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-49732

```

```

Query Match 17.0%; Score 160.4; DB 8; Length 201;
Best Local Similarity 97.7%; Pred. No. 6.4e-31;
Matches 172; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 428 AGAAGGACTTCCTCCGAGAGCGGCGGAGAGCAAGCAAGATGCGGCAAAAGCTCA 487
DB 26 AGAAGGACTTCCTCCGAGAGCGGCGGAGAGCAAGCAAGATGCGGCAAAAGCTCA 85
QY 488 GCTGAGCGGAGTCTTCAGATCCTGATGAGATCGAACTTGGGAGGGAGACTCGGCC 547
DB 86 GCTGAGCGGAGTCTTCAGATCCTGATGAGATCGAACTTGGGAGGGAGACTCGGCC 145
QY 548 CCTCCAGTGAATCTTCGATCGATCCGAAA--TCACCCGTTTCCATTTGCCCTGG 602
DB 146 CTTCCAGTGAATCTTCGATCGATCCGAAA--TCACCCGTTTCCATTTGCCCTGG 201

```

RESULT 10

```

US-60-487-610-9558
; Sequence 9558, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9558

```

```

; LENGTH: 156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-9558

```

```

Query Match 16.4%; Score 155.6; DB 8; Length 156;
Best Local Similarity 99.4%; Pred. No. 9.8e-30;
Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 403 AGTGAAGATTGTGAGATCCTTTAAGAGGAGCTTCGCGCCGAGAGCGCGGACCA 462
DB 1 AGTGAAGATTGTGAGATCCTTTAAGAGGAGCTTCGCGCCGAGAGCGCGGACCA 60
QY 463 GCAAGCAGATGCGGCAAGCTCCAGTGAAGCGAGCTTTCAGTCTGTGGATCGG 522
DB 61 GCAAGCAGATGCGGCAAGCTCCAGTGAAGCGAGCTTTCAGTCTGTGGATCGG 120
QY 523 AACTGGGCAAGGAGGAGCTTCGCGCCCTCCAGTGA 558
DB 121 AACTGGGCAAGGAGGAGCTTCGCGCCCTCCAGTGA 156

```

RESULT 11

```

US-60-487-610-49733
; Sequence 49733, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49733
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-49733

```

```

Query Match 13.4%; Score 126.6; DB 8; Length 201;
Best Local Similarity 99.2%; Pred. No. 2.3e-22;
Matches 126; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCCAGACATGTTCCAGATCCAGATTTAGACCGAGTGAAGAGAAAGCTCAAGCTCT 102
DB 75 GCCAGACATGTTCCAGATCCAGATTTAGACCGAGTGAAGAGAAAGCTCAAGCTCT 134
QY 103 GCAGAGAGGAGCTCGGCGCCAGCCCGCAGAGGAGCGGCGCTCAAGCTCGGCAAGCAT 162
DB 135 GCAGAGAGGAGCTCGGCGCCAGCCCGCAGAGGAGCGGCGCTCAAGCTCGGCAAGCAT 194
QY 163 CATGCC 169
DB 195 CATGCC 201

```

RESULT 12

```

US-60-487-610-9559
; Sequence 9559, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0

```

SEQ ID NO 9559
LENGTH: 118
TYPE: DNA
ORGANISM: Homo sapiens
US-60-487-610-9559

Query Match 12.4%; Score 117.6; DB 8; Length 118;
Best Local Similarity 99.2%; Pred. No. 3.8e-20;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 52 ATGTTCCAGATCCAGATTTGAGTCCAGTACGAGAAAGTCCAGTCTGACAGAGG 111
DB 1 ATGTTCCAGATCCAGATTTGAGTCCAGTACGAGAAAGTCCAGTCTGACAGAGG 60

QY 112 GGCCTGGGCCCCGAGCGGCGGAGCGGCGCTCAGGCTCCGCGAAGCATCATGCC 169
DB 61 GGCCTGGGCCCCGAGCGGCGGAGCGGCGCTCAGGCTCCGCGAAGCATCATGCC 118

RESULT 13

US-10-664-025-13836
Sequence 13836, Application US/10664025
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/10/664,025
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US/09/621,976
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 13836
LENGTH: 100
TYPE: DNA
ORGANISM: Homo sapiens
US-10-664-025-13836

Query Match 5.1%; Score 48.2; DB 6; Length 100;
Best Local Similarity 82.7%; Pred. No. 0.013;
Matches 67; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 1 GGGGCTAGGGGGCGGCTCAGAGTGGGCTTGGGCGCAGAGCATGTTCCAG 60
DB 21 GGGAGGCGGCGAGCGCGGCTCAGAGTGGGCTTGGGCGCAGAGCATGTTCCAG 79

QY 61 ATCCAGAGTTTGAGCCGAGT 81
DB 80 ATCCAGAGTTTGAGCCGAGT 100

RESULT 14

US-10-384-245-499/c
Sequence 499, Application US/10384245
GENERAL INFORMATION:
APPLICANT: Alex Chenchik
TITLE OF INVENTION: Antisense RNA Standardizing Control
FILE REFERENCE: CLON-087PRV
CURRENT APPLICATION NUMBER: US/10/384,245
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 1090
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 499
LENGTH: 80
TYPE: DNA
ORGANISM: Rat
US-10-384-245-499

Query Match 5.0%; Score 47.6; DB 7; Length 80;
Best Local Similarity 85.5%; Pred. No. 0.018;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 211 CAGCCACGACGAGCCATCATGAGGCGCTGGGCTGTGAGATCCGAGTCCGAC 270
DB 71 CAGCCACGACGAGCCATCATGAGGCGCTGGGCTGTGAGATCCGAGTCCGAC 12

QY 271 AG 272
DB 11 AG 10

RESULT 15

PCT-US03-30720-69/c
Sequence 69, Application PC/TUS0330720
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Zhiwei
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Jie
APPLICANT: Ghosh, Malabika
APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Chen, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: Polyptides
CURRENT APPLICATION NUMBER: PCT/US03/30720
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: 60/416,186
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: PCT/US01/04941
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 10/084,643
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 2564
SOFTWARE: pf_genes Version 6.0
SEQ ID NO 69
LENGTH: 2182
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (366)..(1628)
PCT-US03-30720-69

Query Match 4.5%; Score 42.2; DB 1; Length 2182;
Best Local Similarity 50.2%; Pred. No. 1.1;
Matches 131; Conservative 0; Mismatches 128; Indels 2; Gaps 1;

QY 67 GAGTTGAGCGGAGTACGAGAAAGTCCAGTCTGACAGAGGCGCTGGGCCCGAC 126
DB 386 GCGCTGAGCGCGGAGCACTTGTCTCATGCTCGGGAGGCGGAGGCGGAGG 327
QY 127 CCGCAGAGGAGCGGCGCTCAGGCTCCGAGAGCATCATGCGAGGCCCGAGGCTTCTG 186

Db	326	GGGCTCCCACTGCTCCCTGAGCCCGCGAGTGCACGCGGGGACCCCGGGGCTCCGG	267
Qy	187	--TGGACCCCACTCAGACAGACAGCAACAGACAGACCATCATGAGGCGCTG	244
Db	266	GAGGGCCCCGGAGTCCCCGGGCTGCTGCGCGGCGCGCTTACCTGCGCGCCC	207
Qy	245	GGGCTGTGAGATCCGAGTCCGACAGCTCTACCCCGGGGACGAGAGAGAGAG	304
Db	206	GGGCTGCGGGCTCGGGAGAGGCCATCGGCCCGGACGGGACGGGGCGGAGCGGG	147
Qy	305	GGATGGGGGAGAGCCCAACC	325
Db	146	CGGGAGGGCTGGGCTGGCC	126

Search completed: December 29, 2003, 22:58:19
Job time : 1650 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 15:12:07 ; Search time 2618 Seconds
(without alignments)
8782.290 Million cell updates/sec

Title: US-10-066-179-1
Perfect score: 946
Sequence: 1 599cctagg9gcgcg9gtca.....gtcgtccaaaaa 946

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_gse_hum:*
18: em_gse_hiv:*
19: em_gse_pin:*
20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_nam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rtd:*
26: em_gse_phg:*
27: em_gse_vrl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	778.2	82.3	1001 13	BQ276268 AGENCOURT
2	776.6	82.1	920 10	BG748558
3	766.4	81.0	867 12	B1917840
4	764.8	80.8	873 10	BG742674

5	758.8	80.2	949 10	BG752050
6	751	79.4	880 12	B1756192
7	749.8	79.3	1005 12	BM919507
8	736	77.8	907 13	BQ933058
9	722.2	76.3	933 12	B1669797
10	719.4	76.0	1024 12	BM811187
11	703	74.3	908 14	CA488765
12	702.4	74.2	767 14	CA426410
13	697.4	73.7	773 12	B1870639
14	692.8	73.2	887 14	CA488397
15	692	73.2	1050 12	BM557474
16	690.4	73.0	889 12	B1757416
17	685.6	72.5	761 12	BM973920
18	678.6	71.7	870 14	CD245697
19	678	71.7	920 13	BQ963001
20	674.8	71.3	1170 12	BM464317
21	674.2	71.3	888 13	BQ216214
22	673.8	71.2	891 9	A1338346
23	672.8	71.1	756 12	B1818504
24	667.4	70.5	807 13	BX415776
25	665.6	70.4	880 13	BQ898089
26	663	70.1	873 10	BG289203
27	661.4	69.9	791 12	BM818638
28	658.2	69.6	885 13	BQ420314
29	656.4	69.4	907 10	BG252766
30	655.2	69.3	804 12	B1836511
31	648.6	68.6	703 13	BX093156
32	647	68.4	777 10	BG749431
33	647	68.4	912 13	B182782
34	641.8	67.8	1125 12	BM805363
35	638.2	67.5	706 10	BG748336
36	635.4	67.2	691 10	BG707618
37	631.2	66.7	727 10	BG149833
38	619	65.4	1100 10	BG282723
39	618.2	65.3	1060 12	BM424198
40	613.2	64.8	923 14	CA495333
41	605	64.0	772 10	BG748347
42	603	63.7	722 9	A1813350
43	599.4	63.4	632 12	BM697322
44	598.8	63.3	685 10	BE265011
45	598	63.2	699 10	BF526519

ALIGNMENTS

RESULT 1
LOCUS BQ276268 1001 bp mRNA linear EST 07-MAY-2002
DEFINITION AGENCOURT 6822576 NIH_MGC_111 Homo sapiens cDNA clone IMAGE:5931955
5' mRNA sequence.
ACCESSION BQ276268
VERSION BQ276268.1 GI:20486476
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1001)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LINC2114 row: b column: 20
High quality sequence stop: 658.

FEATURES
source

Location/Qualifiers
1. .1001
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5931955"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 111"
/note="Organ: prostate; Vector: pOMB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 191 a 328 c 325 g 156 t 1 others

Query Match 82.3%; Score 778.2; DB 13; Length 1001;
Best Local Similarity 94.8%; Pred. No. 1.4e-164;
Matches 871; Conservative 0; Mismatches 38; Indels 10; Gaps 6;

13 CCGGCTCAGGGGCTTCGAGATCGGGCTTGGGCCACATGTTCCAGATCCAGAGTTT 72
6 CCGGGCTCAGGGGCTTCGAGATCGGGCTTGGGCCACATGTTCCAGATCCAGAGTTT 65
73 GAGCCGATGAGCAGGAGAGATCTCCAGCTCTGAGAGAGAGGGGCTGGGCCCAAGCCCGCA 132
66 GAGCCGATGAGCAGGAGAGATCTCCAGCTCTGAGAGAGAGGGGCTGGGCCCAAGCCCGCA 125
133 GGGGAGGGGCTTCAGGCTCCGGCAAGCATATCCAGGCTCCAGGCTCTCTGTGGAGC 192
126 GGGGAGGGGCTTCAGGCTCCGGCAAGCATATCCAGGCTCCAGGCTCTCTGTGGAGC 185
193 GCCAGTCCAGCAGGAGAGAGATCTCCAGCTCTGAGAGAGAGGGGCTGGGCCCAAGCCCGCA 252
186 GCCAGTCCAGCAGGAGAGAGATCTCCAGCTCTGAGAGAGAGGGGCTGGGCCCAAGCCCGCA 245
253 GAGATCCGAGATCCGAGAGATCTCCAGCTCTGAGAGAGAGGGGCTGGGCCCAAGCCCGCA 312
246 GAGATCCGAGATCCGAGAGATCTCCAGCTCTGAGAGAGAGGGGCTGGGCCCAAGCCCGCA 305
313 GAGGAGCCAGGCTTCGAGGCTCCGGCAAGCATATCCAGGCTCCAGGCTCTCTGTGGAGC 372
306 GAGGAGCCAGGCTTCGAGGCTCCGGCAAGCATATCCAGGCTCCAGGCTCTCTGTGGAGC 365
373 CAGGCTATGAGCGGAGAGATCTCCAGGATGAGTGAAGTGTGGACTCTCTTAAGAG 432
366 CAGGCTATGAGCGGAGAGATCTCCAGGATGAGTGAAGTGTGGACTCTCTTAAGAG 425
433 GAGCTTCTCCGCGGAGAGAGATCTCCAGGATGAGTGAAGTGTGGACTCTCTTAAGAG 492
426 GAGCTTCTCCGCGGAGAGAGATCTCCAGGATGAGTGAAGTGTGGACTCTCTTAAGAG 485
493 AGCGAGCTTCAGTCTCTGAGGAGATGAGAACTGGGCAAGGAGAGCTCCGCCCTCC 552
486 AGCGAGCTTCAGTCTCTGAGGAGATGAGAACTGGGCAAGGAGAGCTCCGCCCTCC 545
553 CAGTGAACCTTGGTGCATCCGAGAA-TCCACCCGTTCCCATTTGCTGGGAGAGCATT 611
546 CAGTGAACCTTGGTGCATCCGAGAA-TCCACCCGTTCCCATTTGCTGGGAGAGCATT 605
612 TTGAATATGAGAGAGAGTTCCTCTAGGCTTATGCAAAAAGAGAGATCCGTGTAT 671
606 TTGAATATGAGAGAGTTCCTCTAGGCTTATGCAAAAAGAGAGATCCGTGTAT 664
672 CTTTGGAGGAGGTTGAGCCAGATTCCTTCCGCTGTGAGAGAGAGAGAGG-TT 730
665 CTTTGGAGGAGGTTGAGCCAGATTCCTTCCGCTGTGAGAGAGAGAGAGG-TT 724
731 GATCCATCGAAGTTTGGGTTTCCGCCCAAGCCCGAGAGAGTGGCTCCGTGCCCC 790

Db 725 GGTCCATCGGAGAGTTTGGGTTTCCGCCACAGCCCGGAGAGTGGCTCCGGGCC 784
791 GCCCTCAGGTTCCGGGTTTCCGCC--AGGCGCTGCGTAAAGAGAGAGAGTT-- 846
785 GCCCTCAGGTTCCGGGTTTCCGCC--AGGCGCTGCGTAAAGAGAGAGAGTTT 844
847 AACCGTGTGTCACCGGAGCCCGAGCCCGGATGCGC--TGGGGCGGTGATCAGTA 903
845 ACCGTGCGGTACCGGAGCCCGAGCCCGGATGCGC--TGGGGCGGTGATCAGTA 904
904 CCAATGTATTAAGCC 922
905 CCAATGTATTAAGCC 923

RESULT 2
BG748558 920 bp mRNA linear EST 15-MAY-2001
LOCUS 602706251F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842996 5',
DEFINITION mRNA sequence.
ACCESSION BG748558
VERSION BG748558.1 GI:14059211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 920)
NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM1678 row: e column: 13
High quality sequence stop: 899.
Location/Qualifiers
1. .920
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4842996"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 43"
/note="Organ: eye; Vector: pOMB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 180 a 303 c 290 g 147 t

Query Match 82.1%; Score 776.6; DB 10; Length 920;
Best Local Similarity 94.6%; Pred. No. 3.3e-164;
Matches 871; Conservative 0; Mismatches 39; Indels 11; Gaps 6;

28 CGAGATCGGGCTTGGGCCAGAGATTCAGATCCAGAGTTGAGCGAGTGAAGCAG 87
2 CGAGATCGGGCTTGGGCCAGAGATTCAGATCCAGAGTTGAGCGAGTGAAGCAG 61
88 GAAGATTCAGCTTGAAGAGAGGGGCTGGGCCCAAGCCCGAGAGAGAGGCTCTCA 147

Db 62 GAAGACTCCAGCTCTCAGAGAGAGGCGCTGGGCCCCAGCCCGCGAGG39A CGGGCCCTCA 121
 Qy 148 GGCCTCCGGAAGCATCATGCGCCAGGCGCCCTCTGTGGAGCCCATGACAGCAG 207
 Db 122 GGCCTCCGGAAGCATCATGCGCCAGGCGCCCTCTGTGGAGCCCATGACAGCAG 181
 Qy 208 GAGCAGCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 267
 Db 182 GAGCAGCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 241
 Qy 268 CACAGCTCTTACCCCGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
 Db 242 CACAGCTCTTACCCCGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
 Qy 328 TTTCCGGGCGCGCTCGGCGCTCGGCGCGCCCAACCTCTGGGCAAGCAGCGCTATGGCGCG 387
 Db 302 TTTCCGGGCGCGCTCGGCGCTCGGCGCGCCCAACCTCTGGGCAAGCAGCGCTATGGCGCG 361
 Qy 388 GAGCTTCGGAGAGATGATGACGAGATTTGTGACCTCTTTAAGAGGAGCTTCTCGCGCG 447
 Db 362 GAGCTTCGGAGAGATGATGACGAGATTTGTGACCTCTTTAAGAGGAGCTTCTCGCGCG 421
 Qy 448 AAGAGCGCGGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 507
 Db 422 AAGAGCGCGGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 481
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 Db 482 TCCGTGTGGAGATCGGAATTTGGGAGAGGAGAGCTCCGCCCTCCAGTGAAGCTTGGTGC 541
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 Db 542 CACATCCCGGAAA-TCACACCGCTTCCCATTTGCGGCGAGCAGATTTGAATATGGAGAGA 601
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 Db 602 AGT-ACCTTCCTCAGAGCCTATGCAAAAAGAGATCCGTGCTATCTTTGAGAGAGAG 660
 Qy 687 TTGACCCAGATTCCTTCGGGT 745
 Db 661 CTGACCCAGATTCCTTCGGGT 720
 Qy 746 TTTGGGTTTTCCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 805
 Db 721 TTTGGGTTTTCCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
 Qy 806 GCTTTCCCGCAGGCGCTGCGCT-AAATAGCAGAGCAGGTTTAACTGTTGTGTCAACGGG 864
 Db 781 GCTTTCCCGCAGGCGCTGCGCTAAAGTGTGCGAGCAGGTTTAACTGTTGTGTCAACGGG 840
 Qy 865 ACCGAGCGCGCGCAGATGCGCTGTGGGCGCGTATCATGTAACCAATTTAAAGCCCGC 924
 Db 841 ACCGAGCGCGCGCAGATGCGCTGTGGGCGCGTATCATGTAACCAATTTAAAGCCCGC 893
 Qy 925 GTGTGTGCAAAAAA 945
 Db 894 GTGTGTGCAAAAAA 914
 RESULT 3
 LOCUS B1917840 867 bp mRNA linear EST 17-OCT-2001
 DEFINITION 601819366P1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5247712 5',
 mRNA sequence.
 ACCESSION B1917840
 VERSION B1917840.1 GI:16199769
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 (bases 1 to 867)
 NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: L16M1625 row: d column: 17
 High quality sequence stop: 831.
 Location/Qualifiers
 1. 867
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 /mol_type="mRNA"
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 /clone="IMAGE:5247712"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI;
 Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb. Insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH MGC Library."
 BASE COUNT 155 a 290 c 284 g 138 t
 ORIGIN
 Query Match 81.0%; Score 766.4; DB 12; Length 867;
 Best Local Similarity 96.4%; Pred. No. 6.4e-162;
 Matches 827; Conservative 0; Mismatches 26; Indels 5; Gaps 4;
 Qy 21 GGGGGCTGAGATCGGGGCTTGGGCGCCAGAGATGTTCCAGATCCAGATTTGACCCGAG 80
 Db 1 GGGGGCTGAGATCGGGGCTTGGGCGCCAGAGATGTTCCAGATTTGACCCGAG 60
 Qy 81 TGAGCAGAGAGACTCAGCTCTGACAGAGAGGCGCTGGGCCCCAGCCCGAGGAGAGCG 140
 Db 61 TGAGCAGAGAGACTCAGCTCTGACAGAGAGGCGCTGGGCCCCAGCCCGAGGAGAGCG 120
 Qy 141 GCCCTCAGGCTTCGGCAAGCATATGCGCAGGCCCGCAGGCTCTGTGGAGCGCAGTCA 200
 Db 121 GCCCTCAGGCTTCGGCAAGCATATGCGCAGGCCCGCAGGCTCTGTGGAGCGCAGTCA 180
 Qy 201 CCAAGAGAGAGAGCCAGCAGCAGAGCCTATCATAGAGGCGCTGGGCGCTGTGGAATCCG 260
 Db 181 CCAAGAGAGAGAGCCAGCAGCAGAGCCTATCATAGAGGCGCTGGGCGCTGTGGAATCCG 240
 Qy 261 GAGTGCAGCAGCTCTACCCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 320
 Db 241 GAGTGCAGCAGCTCTACCCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 300
 Qy 321 CAGCCCTTTTGGGGCGCGCTCGCGCTCGCGCGCCCAACCTCTGGGAGAGCAGCGCTA 380
 Db 301 CAGCCCTTTTGGGGCGCGCTCGCGCTCGCGCGCCCAACCTCTGGGAGAGCAGCGCTA 360
 Qy 381 TGGCGGCGAGCTTCGGAGAGATGATGAGATTTGTGACCTCTTTAAGAGAGAGCTTCC 440
 Db 361 TGGCGGCGAGCTTCGGAGAGATGATGAGATTTGTGACCTCTTTAAGAGAGAGCTTCC 420
 Qy 441 TGGCGGAGAGAGCGGCGAGCAGCAGCAGATGCGGCAAGCTCAGCTGAGCAGCGAGT 500
 Db 421 TGGCGGAGAGAGCGGCGAGCAGCAGCAGATGCGGCAAGCTCAGCTGAGCAGCGAGT 480
 Qy 501 CTTCCAGTCTGTGTGAGATCGGAATTTGGGAGAGGAGAGCTCCGCCCTCCAGTGAAC 560
 Db 481 CTTCCAGTCTGTGTGAGATCGGAATTTGGGAGAGGAGAGCTCCGCCCTCCAGTGAAC 540

QY 561 TTCGGTCCACATCCCGAAA-TCACCCGCTTCCATTGCGCGAGCCATTGTAATAT 619
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 QY 620 GGGAGGAAGTAAAGTTCCCTCAGGCGCTATGCAAAAAGAGATCCGCTGTAATCTTTGGA 679
 Db 601 GGGGCGGAAGT-ACCTTCCCTCAGGCGCTATGCAAAAAGAGATCCGCTGTAATCTTTGGA 659
 QY 680 GGGAGGCTGAACCAAGATTCCTTCC-AGTGTGTGTAGAGCAGAGAGG--TTGTGTCC 736
 Db 660 GGGAGGCTGAACCAAGATTCCTTCCGAGGTGTGTAGAGCAGAGAGGCTTGTGTCC 719
 QY 737 ATCCGAAGTTTGGGTTTCCGCGCACAGCGCGCGGAAGTGGCTCCGTGCGCGCGCTC 796
 Db 720 ATCCGAAGTTTGGGTTTCCGCGCACAGCGCGCGGAAGTGGCTCCGTGCGCGCTC 779
 QY 797 AGGTTCCGGGTTTCCCGAGCGCTGCGCTTAAGTACGAGCCAGGTTTAACGGTTGTG 856
 Db 780 AGGCTCCGGGCTTTCCCGAGCGCTGCGCTTAAGTACGAGCCAGGTTTAACGGTTGTG 839
 QY 857 TCACCGGAGCCCGAGCCC 874
 Db 840 TCACCGGAGCCCGAGCCC 857

RESULT 4
 LOCUS BG742674 873 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602633280F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778730 5',
 mRNA sequence.
 ACCESSION BG742674
 VERSION BG742674.1 GI:14053327
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 873)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT Contact: Robert Strausberg, Ph.D.
 Email: cgapbsf@mail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLND at:
 http://image.llnl.gov
 Plate: LLMD10634 row: 0 column: 19
 High quality sequence stop: 858.
 Location/Qualifiers
 1. 873
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4778730"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI CGAP Skn3"
 /note="Organ: Skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 158 a 289 c 289 g 137 t
 ORIGIN
 Query Match 80.8%; Score 764.8; DB 10; Length 873;
 Best Local Similarity 96.6%; Pred. No. 1.5e-161;
 Matches 835; Conservative 0; Mismatch 22; Indels 7; Gaps 5;
 QY 12 GCCGGGTGACGGGCTTCGAGATCGGGCTTGGGCCAGAGATGTCAGATCCAGAGTT 71

Db 12 GCCGGGTGACGGGCTTCGAGATCGGGCTTGGGCCAGAGATGTCAGATCCAGAGTT 71
 QY 72 TGAGCCGAGTGAAGAGAAATCTCCAGCTGTGAGAGAGGGGCTGGGCCCAAGCCCGC 131
 Db 72 TGAGCCGAGTGAAGAGAAATCTCCAGCTGTGAGAGAGGGGCTGGGCCCAAGCCCGC 131
 QY 132 AGGAGGAGGGGCTCAGGCTCCGCAAGATCAATCCAGAGCCCAAGGCTCTGTGGGA 191
 Db 132 AGGAGGAGGGGCTCAGGCTCCGCAAGATCAATCCAGAGCCCAAGGCTCTGTGGGA 191
 QY 192 CGCCAGTCCAGCAGAGAGAGCCACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 251
 Db 192 CGCCAGTCCAGCAGAGAGAGCCACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 251
 QY 252 GGAATCCGAGAGTCCAGCAGCTCTAATCCCGGGGGGAGAGAGAGAGAGAGAGAGAG 311
 Db 252 GGAATCCGAGAGTCCAGCAGCTCTAATCCCGGGGGGAGAGAGAGAGAGAGAGAGAG 311
 QY 312 GGAAGAGCCAGCCCTTTGCGGGGCGCTGCGCTCGGCGCCCGCCCAACTCTGGGAGC 371
 Db 312 GGAAGAGCCAGCCCTTTGCGGGGCGCTGCGCTCGGCGCCCGCCCAACTCTGGGAGC 371
 QY 372 ACAGCGCTATGGCCGCGAGCTCCGAGAGATGATGACGAGTTGTGACTCTTTAAGAA 431
 Db 372 ACAGCGCTATGGCCGCGAGCTCCGAGAGATGATGACGAGTTGTGACTCTTTAAGAA 431
 QY 432 GGGAGCTTCGCGCCGAGAGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
 Db 432 GGGAGCTTCGCGCCGAGAGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
 QY 492 GAGCGAGTCTTCAGAGTCTGTGTGGATCGGAACTTGGGAGAGGAGAGTCCGCGCCCTC 551
 Db 492 GAGCGAGTCTTCAGAGTCTGTGTGGATCGGAACTTGGGAGAGGAGAGTCCGCGCCCTC 551
 QY 552 CGAGTACCTTTGGTCCATCCCGAAA-TCACCCGTTTCCATTGCTGGGAGCCAT 610
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 QY 611 TTGAATATGGGAGAGTAAAGTTCCCTCAGGCGCTATGCAAAAAGAGATCCGCTGTA 670
 Db 612 TTGAATATGGGAGAGTAAAGTTCCCTCAGGCGCTATGCAAAAAGAGATCCGCTGTA 670
 QY 671 TCCCTTGAAGAGAGGTTGACCCAGATTCCTTCCGCTGTGTGAAGCCAGAGAG-- 728
 Db 671 TCCCTTGAAGAGAGGTTGACCCAGATTCCTTCCGCTGTGTGAAGCCAGAGAG-- 728
 QY 729 TTGCTCCATCGGAAGTTTGGG--TTTTCGCGCACAGCCCGCGGAAGTGGCTCGTGG 786
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 QY 731 TGAGTCCCATCGGAAGTTTGGGTTTTCAGGCCACAGCCGCGGAAGTGGCTCGTGG 790
 Db 731 TGAGTCCCATCGGAAGTTTGGGTTTTCAGGCCACAGCCGCGGAAGTGGCTCGTGG 790
 QY 787 CCGCGCCCTCAGGTTCCGGGGTTTCCCGCAGGCGCTGAGTATGCGAGCCAGGTTT 846
 Db 787 CCGCGCCCTCAGGTTCCGGGGTTTCCCGCAGGCGCTGAGTATGCGAGCCAGGTTT 846
 QY 791 CCGCGCCCTCAGGTTCCGGGGTTTCCCGCAGGCGCTGAGTATGCGAGCCAGGTTT 850
 Db 791 CCGCGCCCTCAGGTTCCGGGGTTTCCCGCAGGCGCTGAGTATGCGAGCCAGGTTT 850

RESULT 5
 LOCUS BG752050 949 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602732035F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875632 5',
 mRNA sequence.
 ACCESSION BG752050
 VERSION BG752050.1 GI:14062703
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 949)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: LLM11487 row: e column: 09
 High quality sequence stop: 840.

FEATURES
 source

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 /db_xref="taxon:9606"
 /clone="IMAGE:4875632"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_43"
 /note="Organ: eye; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library." |

BASE COUNT 193 a 305 c 299 g 152 t

ORIGIN

Query Match 80.2%; Score 758.8; DB 10; Length 949;
 Best Local Similarity 93.0%; Pred. No. 3.2e-160;
 Matches 863; Conservative 0; Mismatches 52; Indels 13; Gaps 6;

QY 22 GGGCCCTCGAGATCGGGCTTGGGCGCCAGAGCATGTCACATGCCAGTTTACCGCACT 81
 DB 10 GGGCCCTCGAGATCGGGCTTGGGCGCCAGAGCATGTCACATGCCAGTTTACCGCACT 69
 QY 82 GAGCAGAAAGACTCTCAGCTCTGACAGAGAGGGGCTGGGCGCCAGCGGAGCGG 141
 DB 70 GAGCAGAAAGACTCTCAGCTCTGACAGAGAGGGGCTGGGCGCCAGCGGAGCGG 129
 QY 142 CCTCAGGCTCGGCAAGATCATGCGCAGGCGCCAGGCTCTCTGTGGAGCGCCACTGAC 201
 DB 130 CCTCAGGCTCGGCAAGATCATGCGCAGGCGCCAGGCTCTCTGTGGAGCGCCACTGAC 189
 QY 202 CAGCAGAGAGCAACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261
 DB 190 CAGCAGAGAGCAACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 249
 QY 262 AGTCGCAAGCTCTCAGCTCTGACAGAGAGGGGAGAGAGAGAGAGAGAGAGAGAGAG 321
 DB 250 AGTCGCAAGCTCTCAGCTCTGACAGAGAGGGGAGAGAGAGAGAGAGAGAGAGAGAG 309
 QY 322 AGCCCTCTTGGGGCGGCTCGGCGCTCGGCGCCCAACCTCTGTGGAGAGAGAGAG 381
 DB 310 AGCCCTCTTGGGGCGGCTCGGCGCTCGGCGCCCAACCTCTGTGGAGAGAGAGAGAG 369
 QY 382 GGGCGGAGAGCTCGGAG 441
 DB 370 GGGCGGAGAGCTCGGAG 429
 QY 442 GGGCGGAG 501
 DB 430 GGGCGGAG 489
 QY 502 TTCCAGTCTGTGGATCGAACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 561
 DB 490 TTCCAGTCTGTGGATCGAACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549

QY 562 TCGGTCACATCCCGGAA-TCCACCGGTTCCCATGGCCCTGGGAGAGCATTTGAATATG 620
 DB 550 TGGCTCCACATCCCGAACTCCACCGGTTCCCATGGCCCTGGGAGAGCATTTGAATATG 609
 QY 621 GGAGGAGTAAAGTTCCCTCAGGCTATGCAAAAGAGATCCGTGTATCTTTGGAG 680
 DB 610 GGCGGAAAGT-ACCTCCCTCAGGCTATGCAAAAGAGATCCGTGTATCTTTGGAG 668
 QY 681 GGAGGTTAAACCAATTCCTTCGGGTGTGTGTGAAGCAGGAA--GGTTGGTCCAT 738
 DB 669 GGAGGCTGAGCCCAATTCCTTCGGGTGTGTGTGAAGCAGGAAAGGCTTGTCCCAT 728
 QY 739 CGAAGTTTGGGTTTCCGCCACAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798
 DB 729 CGAAGTTTGGG---TTTCGCCACAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 785
 QY 799 GTTCCGGGTTTCCCGCAGGCGCTGCGCTAAGTACGAGCCAGGTTTAAACGTTGTGTC 858
 DB 786 GTTCCGGGCTTTCGCCAGGCGCTGCGCTAAGTACGAGCCAGGTTTAAACGTTGTGTC 844
 QY 859 ACCGGAGACCGAGCGCCGCGATGCCCTGGGGCGCTGTATCATACCAATTTAATATA 918
 DB 845 CACCGGAGACCGAGCGCC---GGATGCCCTGGGGCGCTGTATCATACCAATTTAATATA 899
 QY 919 GCGCGGTGTGCGCAAAAAAAAAAAAAA 946
 DB 900 GCGGTGTGTGCGCAAAAAAAAAAAAAA 927

RESULT 6
 B1756192 880 bp mRNA linear EST 25-SRP-2001
 LOCUS 60302421111 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194731 5',
 DEFINITION mRNA sequence.
 ACCESSION B1756192
 VERSION B1756192.1 GI:15747770
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 880)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: LLM11487 row: e column: 04
 High quality sequence stop: 880.

FEATURES
 source

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 /db_xref="taxon:9606"
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 /lab_host="DH10B"
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 /note="Organ: Brain; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research tracking code 019. Note:

BASE COUNT 158 a 293 c 289 g 140 t
 this is a NIH MGC Library."

Query Match 79.4%; Score 751; DB 12; Length 880;
 Best Local Similarity 96.8%; Pred. No. 1.8e-158;
 Matches 841; Conservative 0; Mismatches 20; Indels 8; Gaps 7;

12 GCCGGGTGAGGGGGCTCGAGATCGGGCTTGGGGCCAGAGACATGTTCCAGATCCAGAGATT 71
 Db 7 GCCCGGGTCAGGGGGCTCGAGATCGGGCTTGGGGCCAGAGACATGTTCCAGATCCAGAGATT 66
 72 TGAAGCCGATGAGCAGAGAACTCCAGCTCTGACAGAGAGAGGGGCTGGGCTCCAGGCTCCG 131
 Db 67 TGAAGCCGATGAGCAGAGAACTCCAGCTCTGACAGAGAGAGGGGCTGGGCTCCAGGCTCCG 126
 132 AGGGGAGCGGGGCTTCAGAGCTCCGGAGACATATGCGAGAGAGAGAGAGAGAGAGAGAGAG 191
 Db 127 AGGGGAGCGGGGCTTCAGAGCTCCGGAGACATATGCGAGAGAGAGAGAGAGAGAGAGAGAG 186
 192 CGCCATCAGCAGCAG 251
 Db 187 CTCAGATACCAAGCAG 246
 252 GAGAGTCGAGAGTCGAG 311
 Db 247 GAGAGTCGAGAGTCGAG 306
 312 GAG 371
 Db 307 GAG 366
 372 ACAGAGCTATGAG 431
 Db 367 ACAGAGCTATGAG 426
 432 GAGAGCTTCTGCGCCGAG 491
 Db 427 GAGAGCTTCTGCGCCGAG 486
 492 GAG 551
 Db 487 GAG 545
 552 CCAG 610
 Db 546 CCAG 605
 611 TTGGAATATGAG 670
 Db 606 TTGGAATATGAG 664
 671 TCCTTTGAG 728
 Db 665 TCCTTTGAG 724
 729 TTGAGCCATGAG 788
 Db 725 TTGAGCCATGAG 782
 789 CGGCGCTCAG 848
 Db 783 CGGCGCTCAG 841
 849 CCGTTGTGTACACCGGAG 877
 Db 842 CCGTTGTGTACACCGGAG 870

RESULT 7
 BM919507 1005 bp mRNA linear EST 12-MAR-2002
 LOCUS BM919507
 DEFINITION AGNCOURT_6761878 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748797

ACCESSION 5', mRNA sequence.
 VERSION BM919507
 XREF GI:19369886
 KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS NIH-MGC
 TITLE NIH-MGC
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Straubeberg, Ph.D.
 Email: cgsab-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM12777 row: c column: 06
 High quality sequence stop: 630.

FEATURES

source

Location/Qualifiers

1..1005
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE:5748797"
 /lab_host="DH10B"
 /clone_id="NIH_MGC_120"
 /note="Organ: pooled pancreas and spleen; Vector: pcwv-sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 YO male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH MGC Library."

BASE COUNT 203 a 324 c 312 g 164 t 2 others
 ORIGIN

Query Match 79.3%; Score 749.8; DB 12; Length 1005;
 Best Local Similarity 95.0%; Pred. No. 3.4e-158;
 Matches 838; Conservative 0; Mismatches 38; Indels 6; Gaps 6;

67 GAGTTGAGCCGAGTGCAG 126
 Db 13 GAGTTGAGCCGAGTGCAG 72
 127 CCGGAGGGGAGCGGGCCCTCAGAGCTCGGGAGAGATGATCGGAGGAGAGAGAGAGAGAGAGAGAG 186
 Db 73 CCGGAGGGGAGCGGGCCCTCAGAGCTCGGGAGAGATGATCGGAGGAGAGAGAGAGAGAGAGAGAG 132
 187 TGGAGCCAGTGCAG 246
 Db 133 TGGAGCCAGTGCAG 192
 247 GCTGTGAGATCGGAGTGCAGAGCTCTTACCCGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
 Db 193 GCTGTGAGATCGGAGTGCAGAGCTCTTACCCGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
 307 ATGGGGAG 366
 Db 253 ATGGGGAG 312
 367 GCAGCAGAGCGCTATGAGCGGAGAGCTCGAGAGATGATGACAGAGTTTGTGAGATCTCTT 426
 Db 313 GCAGCAGAGCGCTATGAGCGGAGAGCTCGAGAGATGATGACAGAGTTTGTGAGATCTCTT 372
 427 AAGAAGGAGCTTCTGCGCCGAGAGAGCGGGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486

Db 373 AAGAGGAGCTTCTGCGCCGGAAGCGGGGACAGCAACGAGATGCGGCAAGCTCC 432
 Qy 487 AGCTGAGCGGAGTCTTCCAGTCTCTGATGAGATCGAACTTGGGAGGGAGCTCGCC 546
 Db 433 AGCTGAGCGGAGTCTTCCAGTCTCTGATGAGATCGAACTTGGGAGGGAGCTCGCC 492
 Qy 547 CCCTCCAGTACCTTCCGATCCAGATCCCGAAA-TCACCCGCTTCCATTTGCCCTGGCA 605
 Db 493 CCCTCCAGTACCTTCCGATCCAGATCCCGAAA-TCACCCGCTTCCATTTGCCCTGGCA 552
 Qy 606 GCCATTTTGAATATGGAGAGAGTAAGTTCCTCAGGCTTATCCAAAAAGAGATCCGTC 665
 Db 553 GCCATTTTGAATATGGAGAGAGTAAGTTCCTCAGGCTTATCCAAAAAGAGATCCGTC 611
 Qy 666 CTGTATCTCTT-TGGAGGAGGGGTGACCCAGATTTCCCTTCCGGTGTGTGAAGCCAG 724
 Db 612 CTGTATCTCTT-TGGAGGAGGGGTGACCCAGATTTCCCTTCCGGTGTGTGAAGCCAG 671
 Qy 725 AAGGTTGATCCGATCCG-AGTTTGGGTTTTCGCGCAAGCCGCG-AGTGGCTCC 782
 Db 672 AAGGTTGATCCGATCCGAAAGTTTGGGTTTTCGCGCAAGCCGCGAAAGTGGCTCC 731
 Qy 783 GTGGGCCCCCTCAGGCTTCCGGGTTTCCCGCAGGCTGCTAAGTAGGAGCCAG 842
 Db 732 GTGGGCCCCCTCAGGCTTCCGGGTTTCCCGCAGGCTGCTAAGTAGGAGCCAG 791
 Qy 843 GTTTAAGCTGTGTGACCGGGACCGGAGCCCGCGGATG-CCCTGGGGGGCGGTGATCAG 901
 Db 792 GTTTAAGCTGTGTGACCGGGACCGGAGCCCGCGGATG-CCCTGGGGGGCGGTGATCAG 851
 Qy 902 TACCAATGTATTAAGCCCGGTGTGTGCAAAAAA 943
 Db 852 TACCAATGTATTAAGCCCGGTGTGTGCAAAAAA 893

RESULT 8 BO933058 907 bp mRNA linear EST 21-AUG-2002
 LOCUS AGENCOURT 8733254 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6454779
 DEFINITION 5', mRNA sequence.
 ACCESSION BO933058
 VERSION BO933058.1 GI:22348441
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 907)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L162632 row: 9 column: 04
 High quality sequence stop: 629.
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 /lab_host="DH10B (phage-resistant)"
 /clone_11b="NIH_MGC_101"
 /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
 XhoI; cDNA made by oligo-dT priming. Directionally cloned

BASE COUNT 179 a 296 c 286 g 146 t
 ORIGIN
 Query Match 77.8%; Score 736; DB 13; Length 907;
 Best Local Similarity 97.1%; Pred. No. 4.3e-155;
 Matches 792; Conservative 0; Mismatches 20; Indels 4; Gaps 4;
 Qy 67 GAGTTTGAACCGAGTGAAGAGAGAGTCTGACAGAGAGGGGCTTGGGCCCCAGC 126
 Db 1 GAGTTTGAACCGAGTGAAGAGAGAGTCTGACAGAGAGGGGCTTGGGCCCCAGC 60
 Qy 127 CCGCAGAGGAGAGGGGCTTCAAGCTTCCGCAAGATCATGCGCAGGCTCCAGGCTCTG 186
 Db 61 CCGCAGAGGAGAGGGGCTTCAAGCTTCCGCAAGATCATGCGCAGGCTCCAGGCTCTG 120
 Qy 187 TGGAGCGCATGATCAG 246
 Db 121 TGGAGCGCATGATCAG 180
 Qy 247 GCTGTGAGATCCGAGAGTGCAGAGCTCTACCCGCGGGAGAGAGAGAGAGAGAGAG 306
 Db 181 GCTGTGAGATCCGAGAGTGCAGAGCTCTACCCGCGGGAGAGAGAGAGAGAGAGAG 240
 Qy 307 ATGGGAG 366
 Db 241 ATGGGAG 300
 Qy 367 GCAGCAG 426
 Db 301 GCAGCAG 360
 Qy 427 AAG 486
 Db 361 AAG 420
 Qy 487 AGCTGAGCGGAGTCTTCCAGTCTGTGGAGATCCGAACTTGGGAGAGAGAGAGAGAG 546
 Db 421 AGCTGAGCGGAGTCTTCCAGTCTGTGGAGATCCGAACTTGGGAGAGAGAGAGAGAG 480
 Qy 547 CCCTCCAGTACCTTCCGATCCAGATCCCGAAA-TCACCCGCTTCCATTTGCCCTGGCA 605
 Db 481 CCCTCCAGTACCTTCCGATCCAGATCCCGAAA-TCACCCGCTTCCATTTGCCCTGGCA 540
 Qy 606 GCCATTTTGAATATGGAGAGAGTAAGTTCCTCAGGCTTATCCAAAAAGAGATCCGTC 665
 Db 541 GCCATTTTGAATATGGAGAGAGTAAGTTCCTCAGGCTTATCCAAAAAGAGATCCGTC 599
 Qy 666 CTGTATCTCTTGAAGAGAGAGTGAACCAAGTTCCTTCCGGTGTGTGAAGCCAGCA 725
 Db 600 CTGTATCTCTTGAAGAGAGAGTGAACCAAGTTCCTTCCGGTGTGTGAAGCCAGCA 659
 Qy 726 AGG-TTGGTCCCATGGAAGTTTGGGTTTCCGCCCAAGCCGCGGAAGTGCCTCGT 784
 Db 650 AGG-TTGGTCCCATGGAAGTTTGGGTTTCCGCCCAAGCCGCGGAAGTGCCTCGT 719
 Qy 785 GGGCCCCGCTCAGGTTCCGGGTTTCCCGCAGGCGCTGAGTGAAGAGAGAGAGAGAG 843
 Db 720 GGGCCCCGCTCAGGTTCCGGGTTTCCCGCAGGCGCTGAGTGAAGAGAGAGAGAGAG 779
 Qy 844 TTTAAGCGTGTGTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
 Db 780 TTTAAGCGTGTGTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 815

RESULT 9 B1669797 933 bp mRNA linear EST 12-SEP-2001
 LOCUS B1669797

DEFINITION 603293376F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312683 5', mRNA sequence.

ACCESSION B1669797

VERSION B1669797.1 GI:15584030

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 933)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palikovit, M.D.; Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Plate: LLM11792 row: g column: 20
High quality sequence stop: 874.

FEATURES

source

1..933
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BASE COUNT 183 a 306 c 299 g 145 t

ORIGIN

Query Match 76.3%; Score 722.2; DB 12; Length 933;
Best Local Similarity 92.5%; Fred. No. 5.4e-152;
Matches 859; Conservative 0; Mismatches 59; Indels 12; Gaps 9;

QY 19 CAGGGGCTCGAGATCGGGCTTGGGCGCAGAGCATGTTCCAGATCCGAGATTGAGCG 78

Db 5 CAGGTGCTTCAGATCGGGCTTGGGCGCAGAGCATGTTCCAGATCCGAGATTGAGCG 64

QY 79 AGTAGAGAGAAGACTCCAGCTCTGACAGAGGGGCTGGGCGCCAGGCCCGCAGGGGAC 138

Db 65 AGTAGAGAGAAGACTCCAGCTCTGACAGAGGGGCTGGGCGCCAGGCCCGCAGGGGAC 124

QY 139 GGGGCTTGAAGCTCGGAGAGCATATGCGAGGCGCCAGGCTCTCTGTGGAGCGCCAGT 198

Db 125 GGGGCTTGAAGCTCGGAGAGCATATGCGAGGCGCCAGGCTCTCTGTGGAGCGCCAGT 184

QY 199 CACGAG 258

Db 185 CACGAG 244

QY 259 CGAGTGCAGCAGCTCTAATCCCGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 318

Db 245 CGAGTGCAGCAGCTCTAATCCCGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 304

QY 319 CCGAGGCTCTTTCGGGGCGGCTCGGCTGGGCGCCCGCAACTCTTGGGAGAGAGAGCG 378

Db 305 CCGAGGCTCTTTCGGGGCGGCTCGGCTGGGCGCCCGCAACTCTTGGGAGAGAGAGCG 364

QY 379 TATGCCCGCAGACTCCGAGAGATGACGAGATTGTGACTCTTTAAGAGGAGACTT 438

Db 365 TATGCCCGCAGACTCCGAGAGATGACGAGATTGTGACTCTTTAAGAGGAGACTT 424

QY 439 CTTGCCCGCAGAGAGCGGGGACAGCAGCAGATGCGGAGAGAGAGAGAGAGAGAGAG 498

Db 425 CTTGCCCGCAGAGAGCGGGGACAGCAGCAGATGCGGAGAGAGAGAGAGAGAGAGAG 484

QY 499 GTCTTCAGCTCGGAGAGATGCGAATTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558

Db 485 GTCTTCAGCTCGGAGAGATGCGAATTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544

QY 559 CTTGCGTCCACATCCCGAAA-TCACCCGTTCCATTGCTCGGAGAGAGAGAGAGAGAG 617

Db 545 CTTGCGTCCACATCCCGAAA-TCACCCGTTCCATTGCTCGGAGAGAGAGAGAGAGAG 604

QY 618 ATGGAG 677

Db 605 ATGGAG 663

QY 678 GAGGAG 735

Db 664 GAGGAG 722

QY 736 CATCGAAGATTGTTGGTTTCCGCCACAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 795

Db 723 CATCGAAGATTGTTGGTTTCCGCCACAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 782

QY 796 CAGTTCCGGGGGTTTCCGCCACAGCGGCTGAGTAAAGAGAGAGAGAGAGAGAGAGAG 855

Db 783 AGGGCTC--GGGCTTCCCGCAGAGGCTGAGTAAAGAGAGAGAGAGAGAGAGAGAGAG 839

QY 856 GTACCGGAG 915

Db 840 GTACCGGAG 895

QY 916 AAGCCCGGCTGTGTGCAAAAAA 944

Db 896 AAGCCCGGCTGTGTGCAAAAAA 924

RESULT 10

BM811187

LOCUS 1024 bp mRNA linear EST 05-MAR-2002

DEFINITION AGENCOURT 6594892 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5465893

ACCESSION 5', mRNA sequence.

VERSION BM811187

KEYWORDS BM811187.1 GI:19128010

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1024)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Plate: LLM1965 row: g column: 14
High quality sequence stop: 644.

FEATURES

source

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Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"


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/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: Skin; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."
BASE COUNT      201 a      333 c      332 g      158 t
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Query Match      76.0%; Score 719.4; DB 12; Length 1024;
Best Local Similarity 96.9%; Pred. No. 2.3e-151;
Matches 819; Conservative 0; Mismatches 16; Indels 10; Gaps 8;
QY 13 CCGGCTCAGGGGCTCGAGATCGGGCTTGGGCCAGAGATGTTCCAGATCCAGAGTTT 72
DB 7 CCGGGTCAGGGGCTCGAGATCGGGCTTGGGCCAGAGATGTTCCAGATCCAGAGTTT 66
QY 73 GAGCCGAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 132
DB 67 GAGCCGAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
QY 133 GGGGAGAGGGGCTTCAGAGCTTCGGCAAGCATTCGCGAGGCCCTCAGGCTCTCTGGAGC 192
DB 127 GGGGAGAGGGGCTTCAGAGCTTCGGCAAGCATTCGCGAGGCCCTCAGGCTCTCTGGAGC 186
QY 193 GCGAGTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
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QY 253 GAGATCCGGAGTCGCCAGAGCTCTAACCAGGGGAGAGAGAGAGAGAGAGAGAGAGAG 312
DB 247 GAGATCCGGAGTCGCCAGAGCTCTAACCAGGGGAGAGAGAGAGAGAGAGAGAGAGAG 306
QY 313 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
DB 307 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366
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QY 721 GGTCCCATCGAGAGTTT--GGGTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
DB 726 GGTCCCATCGAGAGTTTGGGGGTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 785
QY 787 CCCCGCCTCAGAGTTCCGGGG--TTTCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAG 843

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DB 786 CCCCCGCTCGGAGCTCCGGGCTTTCGCCAGAGCGCTGCGGCTAATGCGAGCCAG 845
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DB 846 GTTAA 850
RESULT 11
LOCUS CA488765
DEFINITION AGENCOURT_10808384 MAPCL Homo sapiens cDNA clone IMAGE:6720955 5',
ACCESSION CA488765
VERSION CA488765.1 GI:24951395
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Krieti A. Eglund, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM14281 row: e column: 19
High quality sequence stop: 657.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6720955"
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, LNCaP"
/lab_host="EMDH10B"
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subcloned with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Krieti A. Eglund, James J. Vincent, Robert Strausberg,
Bungkok Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
BASE COUNT      177 a      295 c      291 g      144 t      1 others
ORIGIN
Query Match      74.3%; Score 703; DB 14; Length 908;
Best Local Similarity 94.3%; Pred. No. 1.1e-147;
Matches 794; Conservative 0; Mismatches 41; Indels 7; Gaps 6;
QY 29 GAGATCGGAGCTTGGGCCA-GAGCATGTTCCAGATCCAGAGTTGAGCCGAGAGAGAG 87
DB 1 GAGATCGGAGCTTGGGCCATTTGCAATGTTCCAGATCCAGAGTTGAGCCGAGAGAGAG 60
QY 88 GAAAGCTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147
DB 61 GAAAGCTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 148 GGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
DB 121 GGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
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D	b		181	GAGACGCCAACACACACGACGACCATCATGAGAGCCCTGGCCTGTGAGATTCCGAATCGC	240
Q	y		268	CACAGCTTCTAACC CGCGGGAGCGAGGACGACGAAAGGATGGGGAGAGACCCAGCCCC	327
D	b		241	CACAGCTTCTAACC CGCGGGAGCGAGGACGACGAAAGGATGGGGAGAGACCCAGCCCC	300
Q	y		328	TTTTCGGGGCCGCTGC GCGTGGGCGCCCCCCCACCTCTGGGAGACGACGCGCTAATGGCCGC	387
D	b		301	TTTTGGGGCCGCTGC GCGTGGGCGCCCCCCCACCTCTGGGAGACGACGCGCTAATGGCCGC	360
Q	y		388	GAGCTCCGSAAGATGATGATGACGAGTTTGTTGTGACTCTTTAAGAAGGCACTTCTGC CCG	447
D	b		361	GAGCTCCGSAAGATGATGATGACGAGTTTGTTGTGACTCTTTAAGAAGGCACTTCTGC CCG	420
Q	y		448	AAGAGCGCGGGCACAGCAACGCGAATGCGGCGAAAAGCTTCAGCTGACGCGAGTCTTCAG	507
D	b		421	AAGAGCGCGGGCACAGCAACGCGAATGCGGCGAAAAGCTTCAGCTGACGCGAGTCTTCAG	480
Q	y		508	TTCCTGTGTGGATTCGGAATTGGGGCAGGGGAAGCTTCGCCCTCTCCCATGACTTCGGTC	567
D	b		481	TTCCTGTGTGGATTCGGAATTGGGGCAGGGGAAGCTTCGCCCTCTCCCATGACTTCGGTC	540
Q	y		568	CACATCCCGGAAA-TCCACCCGCTGCCATTTGCGCTGGGAGGCACTTTTAATGAGGAGGA	626
D	b		541	CACATCCCGGAAA-TCCACCCGCTGCCATTTGCGCTGGGAGGCACTTTTAATGAGGAGGA	600
Q	y		627	AGTAAGTTCCCTCAGGCGCTATGC AAAAAGAGATCCGTCTGTATCTTTTGAAGGAGCGG	686
D	b		601	AGT-ACCTCCCTCAGGCGCTATGC AAAAAGAGATCCGTCTGTATCTTTTGAAGGAGCGG	659
Q	y		687	TTGACCCAGATTTCCCTTCCGCTGTGTGTGAAAGCCACCGGAAG-TTGTCCTCATGGAAAT	745
D	b		660	CTGACCCAGATTTCCCTTCCGCTGTGTGTGAAAGCCACCGGAAG-TTGTCCTCATGGAAAT	719
Q	y		746	TTTGGGTTTTCCCGCCACAG-CGCGCGGAGATGAGCTCGTGCGCCCGGCTCAGATTCCG	804
D	b		720	TTTTGGGTTTTCCCGCCACAG-CGCGCGGAGATGAGCTCGTGCGCCCGGCTCAGATTCCG	779
Q	y		805	GGGTTTTCCCGCGAGCGCTGCGCTAAGTAGC--GAGCCAGGTTTAAACGTTGTGTCAACG	862
D	b		780	GGCTTTTCCCGAGGGCGCTCGGGGCGCTAATCCCGAAGCCAGGTTAAACGTTGTGTCAAC	839
Q	y		863	CG 864	
D	b		840	CG 841	
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DEFINITION	UI-H-FE1-beh-o-07-0-UI.s1 NCI CGAP FE1 Homo sapiens cDNA clone	767 bp	mRNA	linear	EST 07-NOV-2002
VERSION	CA426410				
KEYWORDS	CA426410.1 GI:24789136				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 767)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
JOURNAL	Tumor Gene Index				
COMMENT	Unpublished				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapdb-remail.nih.gov				
	Tissue Procurement: James Martin				
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa				
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: Clone distribution information can be obtained				
	from Dr. M. Bento Soares, bento-soares@iowa.edu				

QY 724 GAAG-TTGGTCCATCGAAGTTTGGGTTTCCGCCACAGCCCGGAAAGTGCTCC 782
 DB 228 GAAGCTTGCTCCATCGAAGTTTGGGTTTCCGCCACAGCCCGGAAAGTGCTCC 169
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 VERSION BI870639.1 GI:16044312
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNU at:
 http://image.llnl.gov
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 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
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 Note: this is a NIH-MGC library."

BASE COUNT 147 a 247 c 262 g 117 t

ORIGIN

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 mRNA sequence.
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 VERSION CA488397.1 GI:24950179
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Kisti A. Eglund, Ira Pastan
 cDNA Library Preparation: Invitrogen Corp
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNU at:
 http://image.llnl.gov
 Plate: LHAM14279 row: d column: 09
 High quality sequence stop: 664.

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BASE COUNT      163 a      297 c      285 g      142 t
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Best Local Similarity 98.0%; Pred. No. 2.2e-145;
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VERSION    BM557474.1 GI:18799501
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (Dates 1 to 1050)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
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            clone distribution: MGC clone distribution information can be
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Query Match      73.2%; Score 692; DB 12; Length 1050;
Best Local Similarity 97.4%; Pred. No. 3.3e-145;
Matches 746; Conservative 0; Mismatches 15; Indels 5; Gaps 4;
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QY 73 GAGCGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 132
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QY 133 GGGAGCGGGCTCTAGAGCTCTGGCAGAGATATGCGGAGGCGCCGAGGCTCTTGGGAG 192
DB 156 GGGAGCGGGCTCTAGAGCTCTGGCAGAGATATGCGGAGGCGCCGAGGCTCTTGGGAG 215
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Search completed: December 29, 2003, 17:04:15
Job time : 2630 secs

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Davis, Minh-Tam

From: STIC-Biotech/ChemLib
Sent: Tuesday, February 17, 2004 9:35 AM
To: Davis, Minh-Tam
Subject: RE: publication date for a ref for 10/066179

The month of publication is November 15, 1996...from Cell Press, Cambridge Mass. Maude

-----Original Message-----

From: Davis, Minh-Tam
Sent: Sunday, February 15, 2004 11:45 AM
T : STIC-Biotech/ChemLib
Subject: publication date for a ref for 10/066179

Could you check what month is the publication by:

Wang, HG, 1996, Cell 87: 629-638.

Thank you,

MINH TAM DAVIS

ART UNIT 1642,

RESEM ROOM 3A24, MB 3C18

272-8030

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Davis, Minh-Tam

To: STIC-Biotech/ChemLib
Subject: publication date for a ref for 10/066179

Could you check what month is the publication by:

Wang, HG, 1996, Cell 87: 629-638.

Thank you,

MINH TAM DAVIS

ART UNIT 1642,

RESEM ROOM 3A24, MB 3C18

272-8030

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 22:25:19 ; Search time 24 Seconds

(without alignments)
329.187 Million cell updates/sec

Title: US-10-066-179-2

Perfect score: 905
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	649	71.7	204	BAD_MOUSE	Q61337 mus musculu
3	636.5	70.3	205	BAD_RAT	Q35147 rattus norv
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7	92.5	10.2	1082	NC03_RAT	Q9EP02 rattus norv
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11	89.5	9.9	1461	IB18_PRIVIF	P11675 pseudorabie
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ALIGNMENTS

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
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OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
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RN [3]
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RX Wang H.-G., Rapp U.R., Reed J.C.;
RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria";
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RN [5]
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RL "Dimerization properties of human BAD.";
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RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
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 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
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 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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 RP STRUCTURE BY NMR OF 103-127.
 RX MEDLINE=21073561; PubMed=11206074;
 RA Petrov A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,
 RA Mack U., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
 RA Pesik S.W.;
 RT "Rationale for Bcl-xL/Bad peptide complex formation from structure,
 RT mutagenesis, and biophysical studies.";
 RT Protein Sci. 9:2528-2534(2000).
 RL
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
 CC of heterodimerization of these proteins with BAX. Can reverse the
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
 CC similarity). Appears to act as a link between growth factor
 CC receptor signaling and the apoptotic pathways.
 CC
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
 CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
 CC similarity).
 CC
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
 CC phosphorylation, locates to the cytoplasm.
 CC
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC
 CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
 CC BAX for their pro-apoptotic activity and for their interaction
 CC with anti-apoptotic members of the Bcl-2 family.
 CC
 CC -1- PTM: Phosphorylated on Ser-75 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-99 promotes heterodimerization
 CC with 14-3-3 proteins. This interaction then facilitates the
 CC phosphorylation at Ser-118, a site within the BH3 domain, leading
 CC to the release of Bcl-x(L) and the promotion of cell survival.
 CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the
 CC major site of protein kinase A (CAPK) phosphorylation (by
 CC similarity).
 CC
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
 CC in position 64 and 91.
 CC
 CC -----
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 CC -----
 CC
 CC EMBL, U66879; AAB36516.1; ALT_FRAME.
 CC EMBL, AF021792; AAB72092.1; -;
 CC EMBL, AF031523; AAB88124.1; -;
 CC EMBL, BC001901; AAB01901.1; -;
 CC PDB: 1G5J; 07-FEB-01.
 CC
 CC GeneW, HGNC:936; BAD.
 CC
 CC MIM: 603167; -;
 CC
 CC DR GO: 0005737; Cytoplasm; NAS.
 CC DR GO: 0005741; Mitochondrial outer membrane; NAS.
 CC DR GO: 0005515; Protein binding activity; NAS.
 CC DR GO: 0006633; Apoptotic program; TAS.
 CC DR GO: 0006917; Induction of apoptosis; NAS.
 CC InterPro: IPR007112; Bcl2-BH.
 CC PROSITE: PS01259; BH3; FALSE NEG.
 CC DR Apoptosis; Phosphorylation; Polymorphism; 3D-structure.
 CC KX DOMAIN 110 124 BH3.
 CC FT MOD_RES 75 75 PHOSPHORYLATION (BY PKA AND PKB) (BY
 CC FT MOD_RES 99 99 PHOSPHORYLATION (BY PKA AND PKB) (BY
 CC FT MOD_RES 118 118 PHOSPHORYLATION (BY PKA AND PKB) (BY

FT FT SIMILARITY).
 FT VARIANT 107 107 A -> S (in dbSNP:3729933).
 FT FT
 FT HELIX 106 121 /FTid=VAR_015380.
 FT
 SO SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;
 Query Match 100.0%; Score 905; DB 1; Length 168;
 Best Local Similarity 100.0%; Pred. No. 2,6e-62;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MFQIPPEPSEQEDSSAENGGLGSPAGDDPSSGSKHRRAPGLMDASHQOQPTSSSH 60
 Db 1 MFQIPPEPSEQEDSSAENGGLGSPAGDDPSSGSKHRRAPGLMDASHQOQPTSSSH 60
 Oy 61 HGGAGAVEIRSRHSYPAGTEDEDEGMEPEPSPRGRSRAPNLMQAQRGRRLRMSDE 120
 Db 61 HGGAGAVEIRSRHSYPAGTEDEDEGMEPEPSPRGRSRAPNLMQAQRGRRLRMSDE 120
 Oy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDNLGRGSSAPSQ 168
 Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDNLGRGSSAPSQ 168
 RESULT 2
 ID BAD MOUSE STANDARD; PRT; 204 AA.
 AC 061337;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
 DE 6) (Bcl-xL/Bcl-2 associated death promoter).
 GN BAD OR BDC6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Thymus;
 RA MEDLINE=95136361; PubMed=7834748;
 RA Yang B., Zha U., Jockel U., Boise L.H., Thompson C.B., Koremeyer S.J.;
 RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
 RT promotes cell death.";
 RL Cell 80:285-291(1995).
 RN [2]
 RP PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.
 RX MEDLINE=98022383; PubMed=9381178;
 RA Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;
 RT "Interleukin-3-induced phosphorylation of BAD through the protein
 RT kinase Akt.";
 RL Science 278:687-689(1997).
 RN [3]
 RP MUTAGENESIS OF SERINE RESIDUES.
 RX MEDLINE=20403302; PubMed=10949026;
 RA Datta S.R., Katsav A., Hu L., Petrov A., Pesik S.W., Yaffe M.B.,
 RA Greenberg M.E.;
 RT "14-3-3 proteins and survival kinases cooperate to inactivate BAD by
 RT BH3 domain phosphorylation.";
 RL Mol. Cell 6:41-51(2000).
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the
 CC binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
 CC of heterodimerization of these proteins with BAX. Can reverse the
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2.
 CC Appears to act as a link between growth factor receptor signaling
 CC and the apoptotic pathways.
 CC
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
 CC The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.
 CC
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
 CC phosphorylation, locates to the cytoplasm.
 CC
 CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
 CC BAX for their pro-apoptotic activity and for their interaction

CC with anti-apoptotic members of the Bcl-2 family.
 CC -1- PTM: Phosphorylated on Ser-112 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-136 promotes heterodimerization
 CC with 14-3-3 proteins. This interaction then facilitates the
 CC phosphorylation at Ser-155, a site within the BH3 domain, leading
 CC to the release of Bcl-x(L) and the promotion of cell survival.
 CC Ser-136 is the major site of Akt/PKB phosphorylation. Ser-155 the
 CC major site of protein kinase A (CAPK) phosphorylation.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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 CC EMBL: L37296; AAA6465.1; -
 CC DR PIR: A55671; A55671.
 CC DR HSP: G92934; 1G5J.
 CC DR MGI: 1096330; Bad.
 CC DR InterPro: IPR000712; Bcl2_BH.
 CC DR PROSITE: PS01259; BH3; FALSE_NEG.
 CC DR Apoptosis; Phosphorylation.
 CC KM DOMAIN 147 161
 CC FT MOD_RES 112 112 PHOSPHORYLATION (BY PKA AND PKB).
 CC FT MOD_RES 136 136 PHOSPHORYLATION (BY PKA AND PKB).
 CC FT MOD_RES 155 155 PHOSPHORYLATION (BY PKA AND PKB).
 CC FT MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.
 CC FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.
 CC FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH
 CC BCL-X(L).
 CC SQ SEQUENCE 204 AA; 22080 MM; 6C2BA910205053F7 CRC64;
 CC
 CC Query Match 71.7%; Score 649; DB 1; Length 204;
 CC Best Local Similarity 75.6%; Pred. No. 8.3e-43;
 CC Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;
 CC
 CC QY 1 MFQIFEPFSEEDSSAERGLGSPAGGPGSGGKHHQAPQLMDASHOEPRTSSH 60
 CC DB 43 MFQIFEPFSEEDSSAERGLGSPAGGPGSGGKHHQAPQLMDASHOEPRTSSH 97
 CC 61 HGGAGAVETRRSSSSYPACTEDDEGCGEPPRGRSAPNTLMAAGVGEELRMSP 120
 CC DB 98 HGGAGAVETRRSSSSYPACTEDDEGCGEPPRGRSAPNTLMAAGVGEELRMSP 157
 CC QY 121 FVDSFKKGLPRPKSAGTATQMKRSSSWTRVPSWMDRNLRGSSAPSQ 168
 CC DB 156 FEGSF-KGLPRPKSAGTATQMKRSSSWTRVPSWMDRNLRGSSAPSQ 204
 CC
 CC RESULT 3
 CC BAD RAT STANDARD: PRT; 205 AA.
 CC ID BAD RAT 035147; 070256; Q9JHX1.
 CC AC 16-OCT-2001 (Rel. 40; Created)
 CC DT 16-OCT-2001 (Rel. 40; Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41; Last annotation update)
 CC DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
 CC 6) (Bcl-xL/Bcl-2 associated death promoter).
 CC GN BAD.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 CC OX NCBI_Taxid=10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
 CC RC TISSUE=Ovary;
 CC RX MEDLINE=98034386; PubMed=9369453;
 CC RA Hsu S.Y., Kalpita A., Zhu L., Heueh A.J.W.;
 CC RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced

RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
 RL Mol. Endocrinol. 11:1858-1867(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98194755; PubMed=9535132;
 RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
 RT "Cloning and expression of the programmed cell death regulator BAD in
 RT the rat brain.";
 RL Neurosci. Lett. 243:137-140(1998).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RP TISSUE=Brain;
 RC MEDLINE=21109372; PubMed=11161472;
 RA Hamer S., Arumae U., Yu L.-Y., Sun Y.-F., Saarna M., Lindholm D.;
 RT "Functional characterization of two splice variants of rat BAD and
 RT their interaction with Bcl-w in sympathetic neurons.";
 RL Mol. Cell. Neurosci. 17:97-106(2001).
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the
 CC binding to Bcl-x(L). Bcl-2 and Bcl-w, thereby affecting the level
 CC of heterodimerization of these proteins with BAX. Can reverse the
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
 CC similarity). Appears to act as a link between growth factor
 CC receptor signaling and the apoptotic pathways.
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-
 CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
 CC phosphorylation, located to the cytoplasm (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=O35147-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=O35147-2; Sequence=VSP_000534;
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested, including
 CC brain, liver, spleen and heart. In the brain, restricted to
 CC epithelial cells of the choroid plexus. Isoform alpha is the more
 CC abundant form.
 CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
 CC BAX for their pro-apoptotic activity and for their interaction
 CC with anti-apoptotic members of the Bcl-2 family.
 CC -1- PTM: Phosphorylated on Ser-113 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-117 promotes heterodimerization
 CC with 14-3-3 proteins. This interaction then facilitates the
 CC phosphorylation at Ser-156, a site within the BH3 domain, leading
 CC to the release of Bcl-x(L) and the promotion of cell survival.
 CC Ser-137 is the major site of Akt/PKB phosphorylation. Ser-156 the
 CC major site of protein kinase A (CAPK) phosphorylation (By
 CC similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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 CC EMBL: AF003523; AAC53374.1; -
 CC DR EMBL: AF031227; AAC15100.1; -
 CC DR EMBL: AF279910; AAF91427.1; -
 CC DR EMBL: AF279911; AAF91428.1; -
 CC DR HSP: G92934; 1G5J.
 CC DR InterPro: IPR000712; Bcl2_BH.
 CC DR PROSITE: PS01259; BH3; FALSE_NEG.
 CC DR Apoptosis; Phosphorylation; Alternative splicing.
 CC KM DOMAIN 148 162
 CC FT MOD_RES 113 113 PHOSPHORYLATION (BY PKA AND PKB)
 CC FT MOD_RES 148 148 PHOSPHORYLATION (BY PKA AND PKB)
 CC FT MOD_RES 137 137 PHOSPHORYLATION (BY PKA AND PKB)

(BY SIMILARITY).
 PHOSPHORYLATION (BY PKA AND PKB)
 (BY SIMILARITY).
 LPRKSGATATOMSSMTTIIOSMMWRNKGKSGSPSO
 -> EELTVSVFLVRALMGWFLMSFOSEFHTLPPTPP
 EVAMPPLKWTALRLIC (In Isoform Beta).
 /Ftid=VSP_000534.
 S->A: NO EFFECT ON HETERODIMERIZATION
 WITH 14-3-3 PROTEINS.
 S->A: NO HETERODIMERIZATION WITH 14-3-3
 PROTEINS. NO EFFECT ON HETERODIMERIZATION
 WITH BCL2 NOR WITH PROTEIN P11.
 SDAGGR -> ERRGRK (IN REF. 1).
 TAFA71DAE9CF4A81 CRC64;
 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;
 Query Match 70.3%; Score 636.5; DB 1; Length 205;
 Best Local Similarity 75.1%; Pred. No. 7.4e-42;
 Matches 127; Conservative 11; Mismatches 24; Indels 7; Gaps 4;

QY 1 MFOIPEPEPSBOEDSSAERGLGPPAGDGGSGKHROAPGLMDASHQOE-QPTSSS 59
 DQ 43 MFOIPEPEPSBOEDASTTRDGLGSLTDPQ---GPY--LAPGLGSLVQQDPOGAAANS 97
 QY 60 HGGAGAVEIRSRSSYPAGTEDEGMEGEEPSPPGRGSRAPNLMWAQRYGRELRMSD 119
 DQ 98 HGGAGTWTETSRSSYPAGTEDEGMEELSPFRGSRAPNLMWAQRYGRELRMSD 157
 QY 120 EFVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWMDNLGRGSSAPSO 168
 DQ 158 EFEGSP-KGLPRPKSAGTATOMROSSWTRVFQSWMDNLGRGSSAPSO 205

RESULT 4
 W146 HUMAN STANDARD; PRT; 1336 AA.
 ID Q9C0J8;
 AC 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE WD-repeat protein WDC146.
 GN WDC146.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=21092660; PubMed=11162572;
 RA Ito S., Sakai A., Nomura T., Miki Y., Ouchida M., Sasaki J.,
 RA Shimizu K.;
 RT "A novel WD40 repeat protein, WDC146, highly expressed during
 spermatogenesis in a stage-specific manner";
 RL Biochem. Biophys. Res. Commun. 280:656-663(2001).
 CC -1 SUBCELLULAR LOCATION: Nuclear.
 CC -1 TISSUE SPECIFICITY: Most highly expressed in testis.
 CC -1 SIMILARITY: Contains 1 collagenous domain.
 CC -1 SIMILARITY: Contains 7 WD repeats.
 CC -----
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 CC -----
 CC EMBL; AB044749; BAB32435.1; -
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0006301; P:post-replication repair; NAS.
 DR GO; GO:0007283; P:spermatogenesis; NAS.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; Collagen_1.
 DR Pfam; PF00400; WD40; 7.

Prodcm; PD000018; WD40; 2.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR Collagen; Repeat; WD repeat; Nuclear protein.
 FT REPEAT 117 156 WD 1.
 FT REPEAT 159 198 WD 2.
 FT REPEAT 200 239 WD 3.
 FT REPEAT 242 283 WD 4.
 FT REPEAT 286 325 WD 5.
 FT REPEAT 329 369 WD 6.
 FT REPEAT 373 412 WD 7.
 FT DOMAIN 618 770 COLLAGEN-LIKE.
 FT SEQUENCE 1336 AA; 145921 MW; 865E98A2D12381F6 CRC64;
 Query Match 10.8%; Score 98; DB 1; Length 1336;
 Best Local Similarity 24.4%; Pred. No. 4;
 Matches 43; Conservative 16; Mismatches 83; Indels 34; Gaps 7;

QY 3 QIPEPEPSBOEDSSAERGLGPPAGDGGSGKHROAPGLMDASHQOE 53
 DQ 1169 EFPFEGGKAPDSDWGNRERFGHEHFRDTPRPHDPDGHSPASRERSSSLQMDVASL 1228
 QY 54 QPTSSHHGAGAVEIRSRSSYPAGTEDEGMEGEEPSPPGRGSRAPNLMWAQRYGRE 113
 DQ 1229 PPRKRPWHDGPGTSEHREMEA--PGGSEDRG-----GKGRGGPAPQVRPKSGRS 1277
 QY 114 LRMSDFVDSFKKGL--RPKSAGTATOMROSSWTRVFQSWMDNLGRGSSAPPS 167
 DQ 1278 -SSLGDEHHDGYNHDEFGGPGGPGSGTSPGRSGRS-----NWGRGSNNMS 1321

RESULT 5
 CCAA HUMAN STANDARD; PRT; 2505 AA.
 ID CCAA HUMAN
 AC 000555; P78510; P78511; Q16290; Q92690; Q99790; Q99792;
 AC Q99793;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Voltage-dependent P/Q-type calcium channel alpha-1A subunit (Calcium
 DE channel, L type, alpha-1 polypeptide isoform 4) (Brain calcium channel
 DE 1) (BI).
 GN CACNA1A OR CACNA1A4 OR CACNA4 OR CACNA3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCA/GA-1 AND BI-1/LA-2).
 RX MEDLINE=99158614; PubMed=10049321;
 RA Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,
 RA Harpold M.M., Johnson B.C., Williams M.E.;
 RT "Structural elements in domain IV that influence biophysical and
 RT pharmacological properties of human alpha1A-containing high-voltage-
 RT activated calcium channels";
 RL Biophys. J. 76:1384-1400(1999).
 CC (2)
 CC SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS PHM.
 CC TISSUE=Cerebellum;
 CC MEDLINE=97053792; PubMed=8898206;
 RA Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,
 RA Hofmann S.M.G., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E.,
 RA Ferrari M.D., Frans R.R.;
 RT "Familial hemiplegic migraine and episodic ataxia type-2 are caused by
 RT mutations in the Ca2+ channel gene CACNA1A.";
 RL Cell 87:543-552(1996).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 CC TISSUE=Brain;

RA MEDLINE=97141920; PubMed=8988170;
RA Znachenco O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,
RA Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;
RT "Autosomal dominant cerebellar ataxia (SCA6) associated with small
RT polyglutamine expansions in the alpha 1A-voltage-dependent calcium
RT channel.";
RL Nat. Genet. 15:62-69(1997).
RL [4]
RA Lameudin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillewien S.,
RA Phan H., Velaquez N., Do L., Regala M., Terry A., Ganes J.,
RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Altix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coeffield J., Dharé S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommliher B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carraro A.V.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL [5]
RN SEQUENCE OF 1693-1807 FROM N.A.
RN [5]
RX TISSUE=Lung carcinoma;
RX MEDLINE=95123449; PubMed=7623133;
RA Barry E.L.R., Viglione M.P., Kim Y.T., Froehner S.C.;
RT "Expression and antibody inhibition of P-type calcium channels in
RT human small-cell lung carcinoma cells";
RL J. Neurosci. 15:274-283(1995).
RL [6]
RN SEQUENCE OF 2038-2258 FROM N.A.
RN [6]
RX TISSUE=Frontal cortex;
RX MEDLINE=96102310; PubMed=8525433;
RA Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.B.,
RA McInnis M.G., Rose C.A.;
RT "Characterization of cDNA clones containing CCA trinucleotide repeats
RT derived from human brain.";
RL Somat. Cell Mol. Genet. 21:279-284(1995).
RL [7]
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A
CC GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM
CC CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND
CC ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-
CC IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO
CC DIHYDROPYRIDINES (DHP) AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA)
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNIT
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FOR-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoform=7;
CC Comment=Additional isoforms seem to exist;
CC Name=BI-1-GCAG; Synonyms=1A-1;
CC IsoId=000555-1; Sequence=Displayed;
CC Name=BI-1; Synonyms=1A-2;
CC IsoId=000555-2; Sequence=VSP_000875;
CC Name=BI-1(V1);
CC IsoId=000555-3; Sequence=VSP_000871, VSP_000875;
CC Name=BI-1(V1)-GCAG;
CC IsoId=000555-4; Sequence=VSP_000871;
CC Name=BI-1(V2);
CC IsoId=000555-5; Sequence=VSP_000872;
CC Name=BI-1(V2)-GCAG;
CC IsoId=000555-6; Sequence=VSP_000872;
CC Name=BI-1(V2, V3);
CC IsoId=000555-7; Sequence=VSP_000873, VSP_000874;
CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC; MAINLY FOUND IN CEREBELLUM,
CC CEREBRAL CORTEX, THALAMUS AND HYPOTHALAMUS. NO EXPRESSION IN
CC HEART, KIDNEY, LIVER OR MUSCLE. PURKINJE CELLS CONTAIN

CC PREDOMINANTLY P-TYPE VSCC. THE Q-TYPE BEING A PROMINENT CALCIUM
 CC CURRENT IN CEREBELLAR GRANULE CELLS.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC POLYMORPHISM: THE POLY-GLN REGION OF CACNA1A IS POLYMORPHIC: 6 TO
 CC 17 REPEATS IN THE NORMAL POPULATION. EXPANDED TO ABOUT 21 TO 30
 CC REPEATS IN SPINOCEREBELLAR ATAXIA 6 (SCA6) PATIENTS. THERE SEEMS
 CC TO BE A CORRELATION BETWEEN THE REPEAT NUMBER AND EARLIER ONSET OF
 CC THE DISORDER.
 CC -1- DISEASE: Expansion of a CAG repeat in the coding region of CACNA1A
 CC is the cause of one form of spinocerebellar ataxia 6 (SCA6)
 CC [MM:183086], an autosomal dominant disorder characterized by
 CC slowly progressive cerebellar ataxia of the limbs and gait,
 CC dysarthria, nystagmus, and mild vibratory and proprioceptive
 CC sensory loss. These symptoms are probably explained by severe loss
 CC of cerebellar Purkinje cells.
 CC -1- DISEASE: Defects in CACNA1A are the cause of familial hemiplegic
 CC migraine (FHM) [MM:141500]; also known as migraine familial
 CC hemiplegic 1 (MHP1). FHM, a rare autosomal dominant subtype of
 CC migraine with aura, is associated with ictal hemiparesis and, in
 CC some families, progressive cerebellar atrophy.
 CC -1- DISEASE: Defects in CACNA1A are the cause of episodic ataxia type
 CC 2 (BA-2) [MM:108500]; also known as acetazolamide-responsive
 CC hereditary paroxysmal cerebellar ataxia (APCA). This autosomal
 CC dominant disorder is characterized by acetazolamide-responsive
 CC attacks of cerebellar ataxia and migraine-like symptoms,
 CC interictal nystagmus, and cerebellar atrophy.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
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 CC -----
 CC EMBL; AF004884; AAB61613.1; -;
 CC EMBL; AF004883; AAB61612.1; -;
 CC EMBL; X93897; CAA68172.1; -;
 CC EMBL; Z80114.1; NOT_ANNOTATED_CDS.
 CC EMBL; Z80115.1; NOT_ANNOTATED_CDS.
 CC EMBL; U79666; AAB64179.1; -;
 CC EMBL; U79663; AAB49674.1; ALT_INIT
 CC EMBL; U79664; AAB49675.1; ALT_INIT
 CC EMBL; U79665; AAB49676.1; ALT_INIT
 CC EMBL; U79667; AAB49677.1; ALT_INIT
 CC EMBL; U79668; AAB49678.1; ALT_INIT
 CC EMBL; AC005305; AAC26839.1; -;
 CC EMBL; S76537; AAB33068.1; -;
 CC EMBL; U06702.1; NOT_ANNOTATED_CDS.
 CC Genew: HGNC:1388; CACNA1A.
 CC
 CC MIM; 601011; -;
 CC MIM; 183086; -;
 CC MIM; 141500; -;
 CC MIM; 108500; -;
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC GO; GO:0007268; P:synaptic transmission; TAS.
 CC InterPro; IPR001682; Ca/Nb_pore.
 CC InterPro; IPR002077; Ca_channel.
 CC InterPro; IPR002111; Cat_channel_TpPL.
 CC InterPro; IPR005821; Ion_trans.
 CC InterPro; IPR005820; M+channel_nlg.
 CC InterPro; IPR005448; POUCCAlphal.
 CC Pfam; PF00520; ion_trans_4.
 CC PRINTS; PR00167; CACCHANBL.
 CC PRINTS; PR01632; POUCCALPHAL.
 CC CaIc channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC CaIc channel; Glycoprotein; Repeat; Multigene family;

KM Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
 KW Disease mutation; Triplet repeat expansion.
 FT REPEAT 85 363 I.
 FT REPEAT 473 717 II.
 FT REPEAT 1231 1514 III.
 FT REPEAT 1551 1814 IV.
 FT DOMAIN 1 98 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 99 117 S1 OF REPEAT 1 (POTENTIAL).
 FT DOMAIN 118 135 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 136 155 S2 OF REPEAT 1 (POTENTIAL).
 FT DOMAIN 156 167 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 168 185 S3 OF REPEAT 1 (POTENTIAL).
 FT DOMAIN 186 190 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 191 209 S4 OF REPEAT 1 (POTENTIAL).
 FT DOMAIN 210 228 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 229 248 S5 OF REPEAT 1 (POTENTIAL).
 Query Match 10.7%; Score 97; DB 1; Length 2505;
 Best Local Similarity 23.5%; Pred. No. 9.5;
 Matches 48; Conservative 22; Mismatches 54; Indels 80; Gaps 11;
 QY 5 PEPEPSED-----SSAERGLGSP--AGDPSGSGKHHRAP-----42
 DB 2313 PQQQQQQQQQAAVAPGERAATGPRRYGPTAEPLADRPPTGSHSGSRPMERRVPG 2372
 QY 43 -----GLMDAS--HOEOPTSSHHGAGAVEIRSHSSYPAGTEDE---84
 DB 2373 PARSEPPACHGAGRWAPASPHVSEGPGRHIC-----YNGSDYDEADG 2419
 QY 85 ---GNGEE-----PSPPF-----GRS-----RSAPNLMAQRYGRLRMSDEEV 122
 DB 2420 PGSGGGEEMAGAVADAPPVHASSGATGRSPRTFRAGPACASPSRHG---RLPNGYV 2476
 QY 123 DSFKKGLPRKASGATGMRSS 146
 DB 2477 PA--HGLARPGSGRKGLEHPYS 2498
 RESULT 6
 CYAA_NEUCR STANDARD; PRT; 2300 AA.
 ID CYAA_NEUCR STANDARD; PRT; 2300 AA.
 AC Q01631;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenyl
 cyclase).
 GN CR-1 OR NAC.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92000795; PubMed=1680356;
 RA Kore-Bda S., Murayama T., Uno I.;
 RT "Isolation and characterization of the adenylate cyclase structural
 gene of Neurospora crassa.";
 RL Jpn. J. Genet. 66:317-334 (1991).
 CC -1- FUNCTION: Plays essential roles in regulation of cellular
 metabolism by catalyzing the synthesis of a second messenger,
 cAMP.
 CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
 CC -1- COFACTOR: Binds 1 magnesium ion per subunit (by similarity).
 CC -1- SIMILARITY: Belongs to the adenylate cyclase class-3 family.
 CC -1- SIMILARITY: Contains 23 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 P2C-like domain.
 CC -1- SIMILARITY: Contains 1 Ras-associating domain.
 CC -----
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 CC EMBL; D00909; BA00755.1; -
 DR InterPro; IPR001054; G_cyclase.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR001932; P2C-like.
 DR InterPro; IPR000159; RA domain.
 DR Pfam; PF00211; guanylate_cyc; 1.
 DR Pfam; PF00560; LRR; 14.
 DR Pfam; PF00481; P2C; 1.
 DR PRINTS; PR00788; RA; 1.
 DR SMART; SM00044; CYCC; 1.
 DR SMART; SM00362; LRR_TYP; 2.
 DR SMART; SM00314; RA; 1.
 DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
 DR PROSITE; PS50200; RA; 1.
 KW Lyase; Repeat; Leucine-rich repeat; cAMP biosynthesis; Metal-binding;
 KM Magnesium.
 FT DOMAIN 749 841 PAS-ASSOCIATING.
 FT REPEAT 867 890 LRR 1.
 FT REPEAT 892 914 LRR 2.
 FT REPEAT 915 938 LRR 3.
 FT REPEAT 939 961 LRR 4.
 FT REPEAT 962 986 LRR 5.
 FT REPEAT 988 1008 LRR 6.
 FT REPEAT 1009 1031 LRR 7.
 FT REPEAT 1033 1055 LRR 8.
 FT REPEAT 1056 1079 LRR 9.
 FT REPEAT 1081 1097 LRR 10.
 FT REPEAT 1098 1120 LRR 11.
 FT REPEAT 1122 1142 LRR 12.
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 FT REPEAT 8686 8708 LRR 341.
 FT REPEAT 8709 8731 LRR 342.
 FT REPEAT 8732 8754 LRR 343.
 FT REPEAT 8755 8777 LRR 344.
 FT REPEAT 8778 8800 LRR 345.
 FT REPEAT 8801 8823 LRR 346.
 FT REPEAT 8824 8846 LRR 347.
 FT REPEAT 8847 8869 LRR 348.
 FT REPEAT 8870 8892 LRR 349.
 FT REPEAT 8893 8915 LRR 350.
 FT REPEAT 8916 8938 LRR 351.
 FT REPEAT 8939 8961 LRR 352.
 FT REPEAT 8962 8984 LRR 353.
 FT REPEAT 8985 9007 LRR 354.
 FT REPEAT 9008 9030 LRR 355.
 FT REPEAT 9031 9053 LRR 356.
 FT REPEAT 9054 9076 LRR 357.
 FT REPEAT 9077 9099 LRR 358.
 FT REPEAT 9100 9122 LRR 359.
 FT REPEAT 9123 9145 LRR 360.
 FT REPEAT 9146 9168 LRR 361.
 FT REPEAT 9169 9191 LRR 362.
 FT REPEAT 9192 9214 LRR 363.
 FT REPEAT 9215 9237 LRR 364.
 FT REPEAT 9238 9260 LRR 365.
 FT REPEAT 9261 9283 LRR 366.
 FT REPEAT 9284 9306 LRR 367.
 FT REPEAT 9307 9329 LRR 368.
 FT REPEAT 9330 9352 LRR 369.
 FT REPEAT 9353 9375 LRR 370.
 FT REPEAT 9376 9398 LRR 371.
 FT REPEAT 9399 9421 LRR 372.
 FT REPEAT 9422 9444 LRR 373.
 FT REPEAT 9445 9467 LRR 374.
 FT REPEAT 9468 9490 LRR 375.
 FT REPEAT 9491 9513 LRR 376.
 FT REPEAT 9514 9536 LRR 377.
 FT REPEAT 9537 9559 LRR 378.
 FT REPEAT 9560 9582 LRR 379.
 FT REPEAT 9583 9605 LRR 380.
 FT REPEAT 9606 9628 LRR 381.
 FT REPEAT 9629 9651 LRR 382.
 FT REPEAT 9652 9674 LRR 383.
 FT REPEAT 9675 9697 LRR 384.
 FT REPEAT 9698 9720 LRR 385.
 FT REPEAT 9721 9743 LRR 386.
 FT REPEAT 9744 9766 LRR 387.
 FT REPEAT 9767 9789 LRR 388.
 FT REPEAT 9790 9812 LRR 389.
 FT REPEAT 9813 9835 LRR 390.
 FT REPEAT 9836 9858 LRR 391.
 FT REPEAT 9859 9881 LRR 392.
 FT REPEAT 9882 9904 LRR 393.
 FT REPEAT 9905 9927 LRR 394.
 FT REPEAT 9928 9950 LRR 395.
 FT REPEAT 9951 9973 LRR 396.
 FT REPEAT 9974 9996 LRR 397.
 FT REPEAT 9997 10019 LRR 398.
 FT REPEAT 10020 10042 LRR 399.
 FT REPEAT 10043 10065 LRR 400.
 FT REPEAT 10066 10088 LRR 401.
 FT REPEAT 10089 10111 LRR 402.
 FT REPEAT 10112 10134 LRR 403.
 FT REPEAT 10135 10157 LRR 404.
 FT REPEAT 10158 10180 LRR 405.
 FT REPEAT 10181 10203 LRR 406.
 FT REPEAT 10204 10226 LRR 407.
 FT REPEAT 10227 10249 LRR 408.
 FT REPEAT 10250 10272 LRR 409.
 FT REPEAT 10273 10295 LRR 410.
 FT REPEAT 10296 10318 LRR 411.
 FT REPEAT 10319 10341 LRR 412.
 FT REPEAT 10342 10364 LRR 413.
 FT REPEAT 10365 10387 LRR 414.
 FT REPEAT 10388 10410 LRR 415.
 FT REPEAT 10411 10433 LRR 416.
 FT REPEAT 10434 10456 LRR 417.
 FT REPEAT 10457 10479 LRR 418.
 FT REPEAT 10480 10502 LRR 419.
 FT REPEAT 10503 10525 LRR 420.
 FT REPEAT 10526 10548 LRR 421.
 FT REPEAT 10549 10571 LRR 422.
 FT REPEAT 10572 10594 LRR 423.
 FT REPEAT 10595 10617 LRR 424.
 FT REPEAT 10618 10640 LRR 425.
 FT REPEAT 10641 10663 LRR 426.
 FT REPEAT 10664 10686 LRR 427.
 FT REPEAT 10687 10709 LRR 428.
 FT REPEAT 10710 10732 LRR 429.
 FT REPEAT 10733 10755 LRR 430.
 FT REPEAT 10756 10778 LRR 431.
 FT REPEAT

RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Mang K.H., Weitz C., Whitaker C., Winding L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:685-690(2001).
RN [3]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=20300909; PubMed=10823921;
RA Xu J., Liao L., Ning G., Yoshida-Komiyama H., Deng C., O'Malley B.W.,
RT "The steroid receptor coactivator SRC-3 (p/CIP/RAC3/ALB1/ACTR/TRAM-1)
RT is required for normal growth, puberty, female reproductive function,
RT and mammary gland development.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:6379-6384(2000).
CC -1- FUNCTION: Nuclear receptor that directly binds nuclear
CC receptors and stimulates the transcriptional activities in a
CC hormone-dependent fashion. Plays a central role in creating a
CC multisubunit coactivator complex, probably via remodeling of
CC chromatin. Involved in the coactivation of different nuclear
CC receptors, such as for steroids (GR and ER), retinoids (RAR and
CC RXR), thyroid hormone (TRs), vitamin D3 (VDR) and prostanooids
CC (PPARs). Displays histone acetyltransferase activity. Also
CC involved in the coactivation of the NF-kappa-B pathway via its
CC interaction with the NFkB1 subunit (By similarity).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + histone = CoA + acetyl-histone.
CC -1- ENZYME REGULATION: Coactivator activity on nuclear receptors and
CC NF-kappa-B pathways is enhanced by various hormones, and the TNF
CC cytokine, respectively. TNF stimulation probably enhances
CC phosphorylation, which in turn activates coactivator function. In
CC contrast, acetylation by CREBBP apparently suppresses coactivation
CC of target genes by disrupting its association with nuclear
CC receptors (By similarity).
CC -1- SUBUNIT: Interacts with the histone acetyltransferase protein
CC CREBBP. These two proteins are present in a complex containing
CC NCOA2, IKK1, IKK2 and IKK3. Interacts with PCAF (By similarity).
CC -1- SUBCELLULAR LOCATION: Mainly cytoplasmic and weakly nuclear. Upon
CC TNF activation and subsequent phosphorylation, it translocates
CC from the cytoplasm to the nucleus (By similarity).
CC -1- TISSUE SPECIFICITY: Not expressed in all steroid sensitive
CC tissues. Highly expressed in the female reproductive system, in
CC both oocyte and smooth muscle cells of the oviduct, but not
CC expressed in the uterine endometrium. Highly expressed in mammary
CC glands. Expressed moderately in smooth muscle cells of both blood
CC vessels and intestines, and weakly expressed in hepatocytes. In
CC brain, highly expressed in neurons of the hippocampus, and in
CC mural cell and granule layers of the olfactory bulb. Expressed
CC moderately in the internal layer of cerebellum. Not expressed in
CC the spinal chord, cardiac muscle, skeletal muscle, thymus and
CC pancreas.
CC -1- DOMAIN: Contains three leu-Xaa-Xaa-Leu-Leu (LXXLL) motifs. Motifs
CC 1 and 2 are essential for the association with nuclear receptors,
CC and constitute the RID domain (Receptor-interacting domain) (By
CC similarity).
CC -1- PTM: Phosphorylated by IKK complex and acetylated by CREBBP.
CC Acetylation occurs in the RID domain, and disrupts the interaction
CC with nuclear receptors. Both modifications regulate its function
CC (By similarity).
CC -1- MISCELLANEOUS: Defects in NCOA3 result in diverse phenotype of
CC post natal growth retardation, such as dwarfism, delayed puberty,
CC abnormal reproductive function and mammary gland growth
CC retardation.
CC -1- SIMILARITY: BELONGS TO THE SRC/PI60 FAMILY OF NUCLEAR RECEPTOR
CC COACTIVATORS.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -1- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -----
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CC -----
DR EMBL: AF000581; AAC05020.1; -
DR EMBL: AK012229; -; NOT_ANNOTATED_CDS.
DR TRANSFAC: T04638; -
DR MGI: 1276535; Nco3.
DR GO: GO:0005634; C:nucleus; IDA.
DR InterPro: IPR001092; HLH_basic.
DR InterPro: IPR000014; PAS_domain.
DR Pfam: PF00989; PAS; 1.
DR SMART: SM00353; HLH; 1.
DR SMART: SM00091; PAS; 1.
DR PROSITE: PS00038; HLH_1; FALSE_NEG.
DR PROSITE: PS50888; HLH_2; 1.
DR PROSITE: PS50112; PAS; 1.
DR Transferrase: Transcription regulation; Activator; Nuclear protein;
KW Repeat: Acetylation; Phosphorylation.
FT DNA_BIND 36 44 BASIC DOMAIN.
FT DOMAIN 45 81 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 111 181 PAS.
FT DOMAIN 949 1113 INTERACTION WITH CREBBP (BY SIMILARITY).
FT DOMAIN 1104 1278 ACETYLTRANSFERASE ACTIVITY (BY
FT SIMILARITY).
FT DOMAIN 429 664 SER-RICH.
FT DOMAIN 965 987 POLY-GIN.
FT SITE 678 682 LXXLL MOTIF 1.
FT SITE 730 734 LXXLL MOTIF 2.
FT SITE 1041 1045 LXXLL MOTIF 3.
FT MOD_RSS 609 609 ACETYLTATION (BY CREBBP) (BY SIMILARITY).
FT MOD_RSS 612 612 ACETYLTATION (BY CREBBP) (BY SIMILARITY).
FT MOD_RSS 613 613 ACETYLTATION (BY CREBBP) (BY SIMILARITY).
SQ SEQUENCE 1398 AA; 151573 MW; EF4EB92735816C24 CRC64;
Query Match 10.2%; Score 92.5; DB 1; Length 1398;
Beat Local Similarity 25.9%; Pred. No. 11;
Matches 37; Conservative 12; Mismatches 59; Indels 35; Gaps 6;
QY 37 HHRQAPGLVDASHQEQ-----PTSSHHGAGAVIRSHSSYPACTEDDEG 85
DB 1235 HHLQQAAMAMMSQPPQASPPNVTASPSMOCVLGASMPQAPQFPYPA----NYG 1290
QY 86 MGEPSPPGRSRAPNPLMAAQRYGELRMSDEFVDSFRKGLPRKXSGATQMOSS 145
DB 1291 MGQPEPFAFGG--SSPSAMMSMGMSPSONAMVQH-----PQP-----TPMWOPS 1334
QY 146 SWTRVFSWMDRLNGRSSAPSQ 168
DB 1335 D---MKGMPGSGNLARNGSFPQ 1353
RESULT 9
SGL_BOVIN STANDARD; PRT; 646 AA.
AC P23389; 002707;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Secretogranin I precursor (Sgt) (Chromogranin B) (Cgb) [Contains: GAWK
DE peptide; Secretolytin].
GN CHGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
OX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal chromaffin;
RX MEDLINE=91223091; PubMed=2025642;
RA Bauer J.W., Fischer-Colbrie R.,
RT "Primary structure of bovine chromogranin B deduced from cDNA
RL Biochim. Biophys. Acta 1089:124-126(1991).
RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE-Adrenal medulla;
 RX MEDLINE=97282588; PubMed=9136897;
 RA Yoo S.H., Kang Y.K.;
 RT "Identification of the secretory vesicle membrane binding region of
 RL chromogranin B.";
 RM FBS Lett. 406:259-262(1997).
 RP SEQUENCE OF 21-646 FROM N.A.
 RC TISSUE-Adrenal medulla;
 RA Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J.,
 RL Thomas G., Civeill O., Viveros O.H.;
 RM Submitted (Oct-1990) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE OF 634-646.
 RC TISSUE-Adrenal chromaffin;
 RX MEDLINE=95262699; PubMed=7744058;
 RA Strub J.-M., Garcia-Sablone P., Lonnig K., Taupenot L., Hubert P.,
 RL van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;
 RM "Processing of chromogranin B in bovine adrenal medulla.
 RT Identification of secretolytic, the endogenous C-terminal fragment of
 RL residues 614-626 with antibacterial activity.";
 RM Eur. J. Biochem. 229:356-368(1995).
 RP CHARACTERIZATION OF SECRETOLYTIN.
 RX MEDLINE=96184581; PubMed=8603705;
 RA Strub J.-M., Hubert P., Nollans G., Aunis D., Metz-Boutigue M.-H.;
 RL "Antibacterial activity of secretolytin, a chromogranin B-derived
 peptide (614-626), is correlated with peptide structure.";
 RM FBS Lett. 379:273-278(1996).
 RP FUNCTION: SECRETOLYTIN I IS A NEUROENDOCRINE SECRETORY GRANULE
 CC PEPTIDE, WHICH MAY BE THE PRECURSOR FOR OTHER BIOLOGICALLY ACTIVE
 CC PEPTIDES. THE 16 PAIRS OF BASIC AA DISTRIBUTED THROUGHOUT ITS
 CC SEQUENCE MAY BE USED AS PROTEOLYTIC CLEAVAGE SITES.
 CC -1- FUNCTION: SECRETOLYTIN HAS ANTIBACTERIAL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
 CC granules.
 CC -1- PTM: O-GLYCOSYLATED (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE CHROMOGHRANIN / SECRETOGHRANIN PROTEIN
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: X55027; CA38846.1; -;
 DR EMBL: U88551; AAC48720.1; -;
 DR EMBL: X55489; CA39109.1; -;
 DR PIR: S15901; S15901.
 DR InterPro: IPR001819; Chromogranin_AB.
 DR InterPro: IPR001990; Granin.
 DR Pfam: PF01271; Granin.1.
 DR PRINTS: PRO0659; CHROMOGHRANIN.
 DR PROSITE: PS00422; GRANINS_1.1.
 DR PROSITE: PS00423; GRANINS_2.1.
 KM Sulfation: Cleavage on pair of basic residues; signal.
 FT SIGNAL 1 20
 FT CHAIN 21 646
 FT PEPTIDE 418 484 GAWK PEPTIDE.
 FT PEPTIDE 634 646 SECRETOLYTIN.
 FT DISULFID 36 57 BY SIMILARITY.
 FT MOD RES 158 158 SULFATION (POTENTIAL).
 FT MOD RES 315 315 SULFATION (BY SIMILARITY).
 FT CONFLICT 64 64 N -> S (IN REF. 1).
 FT CONFLICT 70 70 N -> D (IN REF. 2).
 FT CONFLICT 93 98 SEAPGL -> FSSPRLS (IN REF. 3).
 FT CONFLICT 181 181 T -> M (IN REF. 2).
 FT CONFLICT 261 261 H -> R (IN REF. 2).
 FT CONFLICT 386 386 P -> R (IN REF. 2).
 FT CONFLICT

FT CONFLICT 481 481 H -> L (IN REF. 3).
 FT CONFLICT 597 597 M -> V (IN REF. 2).
 SO SEQUENCE 646 AA; 73339 MW; 420DB1178FD9E415 CRC64;
 Query Match 9.9%; Score 90; DB 1; Length 646;
 Best Local Similarity 28.7%; Pred. No. 7.3;
 Matches 37; Conservative 16; Mismatches 52; Indels 24; Gaps 6;
 QY 9 PSEODSSAERGLDPSPAGDGPSSGSKH--RQAPGLMDASHQEQP--TSSSHGGA 64
 DB 246 PSESEDA-----SPVDKRRSRPRHHGRSRP---DRSSQDGNPLEESHVGTG 293
 QY 65 GAVEIRSRHSYPACTEDDEGMEGSEPPGRGRSAPPLMAORYGR-----ELRPM 118
 DB 294 NDEKKAHPAHPRLBEGAEYGEVR--RHSAAQAPDGLQARRCGRGSHQALRRS 351
 QY 119 DEFVDSFPK 127
 DB 352 EESLEQENK 360
 RESULT 10
 CCAB HUMAN
 ID CCAB HUMAN STANDARD; PRT; 2339 AA.
 AC 000975;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Voltage-dependent N-type calcium channel alpha-1B subunit (Calcium
 DE channel, L type, alpha-1 polypeptide isoform 5) (Brain calcium channel
 DE II1) (BIII).
 GN CACNA1B OR CACNA1A5 OR CACNA5.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2).
 RC TISSUE-Brain;
 RX MEDLINE=9233686; PubMed=1321501;
 RA Williams M.E., Brust P.F., Feldman D.H., Patchl S., Simerson S.,
 RA Maroufi A., McCue A.F., Veliceteb G., Ellis S.B., Harpold M.M.;
 RT "Structure and functional expression of an omega-conotoxin-sensitive
 RL human N-type calcium channel.";
 RL Science 257:389-395(1992).
 RN (2)
 RP SEQUENCE OF 1-94 FROM N.A.
 RC TISSUE=Lung fibroblast;
 RA Kim D.S., Jung H.H., Park S.H., Chin H.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B
 CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS
 CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
 CC BY (OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY (OMEGA-AGATOXIN-
 CC IIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO
 CC DIHYDROPYRIDINES (DHP), AND (OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
 CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
 CC DIRECTED MIGRATION OF IMMATURE NEURONS.
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE POSE-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha-1B-1;

DT 01-APR-1990 (rel. 14, last sequence update)
 DT 01-FEB-1994 (rel. 28, last annotation update)
 DB Immediate-early protein IE180.
 GN IE.
 OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Alphaherpesvirinae; Varicellovirinae.
 OC NCBI_Taxid=31523;
 RX MEDLINE=89315207; PubMed=2546124;
 RA Cheung A.K.;
 RT "DNA nucleotide sequence analysis of the immediate-early gene of
 RT Pseudorabies virus."
 RL Nucleic Acids Res. 17:4637-4646(1989).
 RN [2]
 RP REVISIONS.
 RA Cheung A.K.;
 RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
 CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
 CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
 CC -1- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
 CC PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
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 CC
 CC EMBL; X15120; CAA3214.1;
 DR InterPro: IPR005205; Herpes_ICP4_C.
 DR InterPro: IPR005206; Herpes_ICP4_N.
 DR Pfam: PF03585; Herpes_ICP4_C; 1.
 DR Pfam: PF03584; Herpes_ICP4_N; 1.
 KM Early protein; Transcription regulation; Trans-acting factor;
 KM DNA-binding; Phosphorylation; Nuclear protein.
 FT DOMAIN 390 405 POLY-SER.
 FT 958 966 POLY-SER.
 SQ SEQUENCE 1461 AA; 14983 MW; 7F31E7ABE403B208 CRC64;

Query Match 9.9%; Score 89.5; DB 1; Length 1461;
 Best Local Similarity 29.4%; Pred. No. 19;
 Matches 50; Conservative 9; Mismatches 70; Indels 41; Gaps 8;

QY 9 PSEODSSAERGLDP--SPAGDG--PSGS---GKHRO-----ARGLMD 47
 DB 211 PARRPASPASPAPGVSAPGGGAPSGGDRGRHHQRREPLDEPAAARLDPPPLCA 290
 QY 48 ASHQEOPTSSSHHGAGAVEIRSRHSYPAGTEDE-----GMCDEPSPRGSRSAF 101
 DB 291 RSPVSSNNSSSSSTTTVAVEPAR-----GREDEDEGLAGDGAFLQGPQRRRAG 344
 QY 102 PNLMAAQRVRELRMSDEFVDS-----FKKGLPRKSAATYQKQSSS 146
 DB 345 E---GALRRGRFPSSSSGSGSDSLSPARSPAPRAAAAAAARSAS 391

RESULT 12
 EVL_MOUSE STANDARD; PRT; 414 AA.
 ID EVL_MOUSE
 AC P70429; Q9ERUB;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Bna/vasodilator stimulated phosphoprotein-like protein (Ena/VASP-like
 DE protein).
 GN EVL.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=97015079; PubMed=8861907;
 RA Gertler F.B., Niebuh K., Reinhard M., Wehland J., Soriano P.;
 RT "Mena, a relative of VASP and Drosophila Enabled, is implicated in the
 RT control of microfilament dynamics."
 RL Cell 87:227-239(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, SUBUNIT, SUBCELLULAR
 RP LOCATION, AND PHOSPHORYLATION BY PKA.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20549629; PubMed=10945997;
 RA Lambrecht A., Kwiatkowski A.V., Lanier L.M., Bear J.E.,
 RA Vandekerckhove J., Ampe C., Gertler F.B.;
 RT "CAMP-dependent protein kinase phosphorylation of EVL, a Mena/VASP
 RT relative, regulates its interaction with actin and SH3 domains."
 RL J. Biol. Chem. 275:36143-36151(2000).
 RN [3]
 RP INTERACTION WITH SEMA6A.
 RX MEDLINE=20564339; PubMed=10993894;
 RA Klostermann A., Lutz B., Gertler F., Behl C.;
 RT "The orthologous human and murine semaphorin 6A-1 proteins
 RT (SEMA6A-1/sem6A-1) bind to the enabled/vasodilator-stimulated
 RT phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
 RT zyxin-like domain."
 RL J. Biol. Chem. 275:39647-39653(2000).
 CC -1- FUNCTION: Enhances actin nucleation and polymerization.
 CC -1- SUBUNIT: Binds to the SH3 domain of Abl1, Lyn and Src. Also binds
 CC to profilin and the WW domain of Apbb1/Fe65. Binds to Sem6a.
 CC -1- SUBCELLULAR LOCATION: Focal adhesions.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=P70429-1; Sequence=Displayed;
 CC -1- PTM: Phosphorylated by PKA; phosphorylation abolishes binding to
 CC SH3 domains of Abl and Src.
 CC -1- SIMILARITY: Contains 1 WH1 domain.
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 CC EMBL; U72519; AAC52862.1;
 DR EMBL; AF279662; AAG23653.1;
 DR PDB; 1OC6; 26-SEP-01.
 DR MGD; MGI:1194884; EVL.
 DR InterPro: IPR006977; EVH1.
 DR InterPro: IPR001960; WH1.
 DR Pfam; PF00568; WH1; 1.
 DR SMART; SMO0461; WH1; 1.
 KM SH3-binding; Phosphorylation; Alternative splicing; 3D-structure.
 FT DOMAIN 1 109 WH1.
 FT 160 204 PRO-RICH.
 FT VARSPLIC 341 361 Missing (in isoform 1).
 FT FTId=VSP 004045.
 SQ SEQUENCE 414 AA; 44337 MW; 146A018BCD6CA370 CRC64;

Query Match 9.8%; Score 89; DB 1; Length 414;
 Best Local Similarity 27.2%; Pred. No. 5.4;
 Matches 41; Conservative 16; Mismatches 56; Indels 38; Gaps 6;

QY 13 EDSSAERGLGSPAGDGPSGSGKHROAPGLMDASHQEOPTSSSHHGAGAVEIRSR 72

Db 237 EDAS-----CGSSPSTGSKS-----DANR-----ASSGCGGGLMEEMNK 271
 Qy 73 -----HSSYPAGTEDEDEGMEEP--SPFRG-RSRAPPLMLMAQYRGRLRMSD 119
 Db 272 LLAARRKAAQTDPKPAKEDENQEDSTSPSPETRATSQPPNSSEGRKPERMSNSVE 331
 Qy 120 EFVDSFKKGLPRPKSAGTATQMRSSSWTRV 150
 Db 332 KPVSSLSTRTPSVAKSPKASPLQSPHSRV 362

RESULT 13

EVL_RAT ID EVL_RAT STANDARD; PRT; 393 AA.
 AC 008719;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ena/Vasodilator stimulated phosphoprotein-like protein (Ena/VASP-like protein).
 GN EVL OR RNB6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=97415794; PubMed=9268706;
 RA Ohta S., Mineta T., Kimoto M., Tabuchi K.;
 RT "Differential display cloning of a novel rat cDNA (RNB6) that shows high expression in the neonatal brain revealed a member of Ena/VASP family.";
 RT Biochem. Biophys. Res. Commun. 237:307-312(1997).
 RL -1- FUNCTION: Enhances actin nucleation and polymerization (By similarity).
 CC -1- SUBUNIT: Binds to the SH3 domains of Abl1, Lyn and Src. Also binds to profilin and the WW domain of Apbb1/Fe65. Binds to Semaph 6 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Focal adhesions (By similarity).
 CC -1- TISSUE SPECIFICITY: Expression detected in brain, spleen, thymus and testis.
 CC -1- DEVELOPMENTAL STAGE: In the brain, expression gradually increases during embryonic development, reaches a maximum at postnatal day 1 and decreases thereafter.
 CC -1- PTM: Phosphorylated by PKA; phosphorylation abolishes binding to SH3 domains of Abl and Src (By similarity).
 CC -1- SIMILARITY: Contains 1 WH1 domain.
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 CC -----
 CC EMBL, U70211; AAC5322.1; -
 DR PIR; JCS614; JCS614.
 DR InterPro; IPR000697; EVH1.
 DR InterPro; IPR001960; WH1.
 DR Pfam; PF00568; WH1; 1.
 DR SMART; SM00461; WH1; 1.
 DR SH3-binding; Phosphorylation.
 FT DOMAIN 1 109
 FT DOMAIN 160 204
 FT SEQUENCE 393 AA; 42095 MW; 6371D91362925D4E CRC64;

Query Match 9.8%; Score 88.5; DB 1; Length 393;
 Best Local Similarity 28.2%; Pred. No. 5.6;
 Matches 40; Conservative 16; Mismatches 45; Indels 41; Gaps 7;

Qy 13 EDSSSAERGLGSPBAGDPSGSGKTHROAPGLMDASHQOEOPTSSHHGAGAVETRSR 72
 Db 237 EDAS-----CGSSPSTGSKS-----DANR-----ASSGCGGGLMEEMNK 271
 Qy 73 -----HSSYPAGTEDEDEGMEEP--SPFRG-RSRAPPLMLMAQYRGRLRMSD 119
 Db 272 LLAARRKAAQTDPKPAKEDENQEDSTSPSPETRATSQPPNSSEGRKPERMSNSVE 331
 Qy 120 EFVDSFKKGLPRPKSAGTATQMRSSSWTRV 141
 Db 332 KPVSSL--LSRYKPAAGVNDV 350

RESULT 14

CMGA_BOVIN ID CMGA_BOVIN STANDARD; PRT; 449 AA.
 AC P05059; P79392;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Chromogranin A precursor (CGA) (Pituitary secretory protein I) (SP-I) [Contains: Vasostatin-1; Chromostatin; Chromacin; Pancreastatin; WE-14; Calcestatin].
 GN CHGA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92140395; PubMed=1779968;
 RA Iacangelo A.L., Grimes M., Eiden L.E.;
 RT "The bovine chromogranin A gene: structural basis for hormone regulation and generation of biologically active peptides.";
 RT Mol. Endocrinol. 5:1651-1660(1991).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86300648; PubMed=3755681;
 RA Benedum U.M., Baerle P.A., Konecki D.S., Frank R., Powell J.,
 RA Mallet J., Kuttner W.B.;
 RT "The primary structure of bovine chromogranin A: a representative of a class of acidic secretory proteins common to a variety of peptidergic cells.";
 RT EMBO J. 5:1495-1502(1986).
 RL [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86311345; PubMed=3018587;
 RA Iacangelo A., Afolter H.-U., Eiden L.E., Herbert E., Grimes M.;
 RT "Bovine chromogranin A sequence and distribution of its messenger RNA in endocrine tissues.";
 RT Nature 323:82-86(1986).
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87260925; PubMed=3474638;
 RA Ahn T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,
 RA Levine M.A.;
 RT "Primary structure of bovine pituitary secretory protein I (chromogranin A) deduced from the cDNA sequence.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
 RL [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97228583; PubMed=9074643;
 RA Kang Y.K., Yoo S.H.;
 RT "Identification of the secretory vesicle membrane binding region of chromogranin A.";
 RT FEBS Lett. 404:87-90(1997).
 RL [6]
 RP SEQUENCE OF 19-45, AND CALCIUM-BINDING.
 RX MEDLINE=90354431; PubMed=2387861;
 RA Yoo S.H., Albanesi U.P.;
 RT "Ca2(+)-induced conformational change and aggregation of chromogranin A.";

RL J. Biol. Chem. 265:14414-14421(1990).

RP SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.

RA MEDLINE=91142185; PubMed=1996343;

RL Galindo E., Rill A., Bader M.-F., Aunis D.;

RT "Chromostatin, a 20-amino acid peptide derived from chromogranin A, inhibits chromaffin cell secretion.";

RT Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).

RM [8]

RM ERRATUM.

RA Galindo E., Rill A., Bader M.-F., Aunis D.;

RL Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).

RM [9]

RP SEQUENCE OF 266-312.

RA MEDLINE=89331945; PubMed=2756155;

RA Nakano I., Funakoshi A., Miyasaka K., Ishida K., Maki G., Angwin P., Chang D., Tatemochi K.;

RT "Isolation and characterization of bovine pancreaticstatin.";

RT Regul. Pept. 25:207-213(1989).

RM [10]

RP SEQUENCE OF 191-212 (CHROMACIN), PHOSPHORYLATION SITE SER-191, AND O-GLYCOSYLATION OF SER-204.

RC TISSUE=chromaffin granules;

RA MEDLINE=97067080; PubMed=8910482;

RA Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M., van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;

RT "Antibacterial activity of glycosylated and phosphorylated chromogranin A-derived peptide 173-194 from bovine adrenal medullary chromaffin granules.";

RT J. Biol. Chem. 271:28533-28540(1996).

RM [11]

RP CHARACTERIZATION OF CATESTATIN.

RA MEDLINE=97439785; PubMed=9294131;

RA Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H., Gill B.M., Parmer R.J.;

RT "Novel autocrine feedback control of catecholamine release. A discrete chromogranin A fragment is a noncompetitive nicotinic cholinergic antagonist.";

RT J. Clin. Invest. 100:1623-1633(1997).

RM [12]

RP CHARACTERIZATION OF CATESTATIN.

RA MEDLINE=99000113; PubMed=9786174;

RA Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;

RT "Mechanism of cardiovascular actions of the chromogranin A fragment catestatin in vivo.";

RT Peptides 19:1241-1248(1998).

RM [13]

RP 3D-STRUCTURE MODELING OF CATESTATIN.

RA MEDLINE=99025667; PubMed=9809795;

RA Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M., Khan I., Parmer R.J., O'Connor D.T.;

RT "Mechanism of action of chromogranin A on catecholamine release: molecular modeling of the catestatin region reveals a beta-strand/loop/beta-strand structure secured by hydrophobic interactions and predictive of activity.";

RT Regul. Pept. 77:43-53(1998).

RM [14]

RP CHARACTERIZATION OF VASOSTATIN-1.

RA MEDLINE=20219105; PubMed=10753865;

RA Lugardon K., Rattner R., Goumon Y., Corti A., Delmas A., Bulet P., Aunis D., Metz-Boutigue M.-H.;

RT "Antibacterial and antifungal activities of vasostatin-1, the N-terminal fragment of chromogranin A.";

RT J. Biol. Chem. 275:10745-10753(2000).

RM [15]

RP CARBOHYDRATE-LINKAGE SITES, PHOSPHORYLATION, AND DISULFIDE BOND.

RA MEDLINE=99459228; PubMed=10527498;

RA Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;

RT "Chromogranin A from bovine adrenal medulla: molecular characterization of glycosylations, phosphorylations, and sequence heterogeneities by mass spectrometry.";

RT Anal. Biochem. 274:69-80(1999).

CC -1- FUNCTION: Pancreasstatin strongly inhibits glucose induced insulin

CC release from the pancreas.

CC -1- FUNCTION: Chromostatin completely inhibits catecholamine release from chromaffin cells.

CC -1- FUNCTION: Chromocin has antibacterial activity against M. luteus.

CC Not active against E. coli.

CC -1- FUNCTION: Catestatin inhibits catecholamine release from chromaffin cells and noradrenergic neurons by acting as a non-competitive nicotinic cholinergic antagonist.

CC -1- FUNCTION: Vasostatin-1 has antibacterial activity against Gram-positive bacteria B. cereus, B. megaterium. Not active against Gram-positive bacteria B. cereus, B. subtilis, S. pyogenes, M. fortuitum, S. aureus and L. monocytogenes and against Gram-negative bacteria E. coli, E. cloacae, S. typhimurium, K. pneumoniae and P. aeruginosa.

CC Possesses antifungal activity against N. crassa, A. fumigatus, A. brassicola, N. hematococcus, F. culmorum and F. oxysporum and against S. cerevisiae and C. albicans yeast. Inactive against T. mentagrophytes.

CC -1- SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory granules.

CC -1- MASS SPECTROMETRY: MW=8584.9; METHOD=MALDI; RANGE=19-94.

CC -1- MISCELLANEOUS: Binds calcium with a low-affinity.

CC -1- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETORANIN PROTEIN FAMILY.

CC -----

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CC -----

DR EMBL: S79270; AAB21297.1; JOINED.

DR EMBL: S79256; AAB21297.1; JOINED.

DR EMBL: S79258; AAB21297.1; JOINED.

DR EMBL: S79260; AAB21297.1; JOINED.

DR EMBL: S79262; AAB21297.1; JOINED.

DR EMBL: S79264; AAB21297.1; JOINED.

DR EMBL: S79266; AAB21297.1; JOINED.

DR EMBL: S79268; AAB21297.1; JOINED.

DR EMBL: X04012; CA27636.1; -.

DR EMBL: X04298; CA27841.1; -.

DR EMBL: M16971; AAA30765.1; -.

DR EMBL: U73523; AAC48700.1; -.

DR PIR: A41520; A41520.

DR PDB: 1GFK; 22-MAR-99.

DR PDB: 1N2Y; 13-NOV-02.

DR GlycoSuiteDB: P05059; -.

DR InterPro: IPR001819; Chromogranin_AB.

DR InterPro: IPR001990; Granin.

DR Pfam: PF01271; Granin; 1.

DR PRINTS: PR00659; CHROMOGRANIN.

DR PROSITE: PS00422; GRANINS_1; 1.

DR PROSITE: PS00423; GRANINS_2; 1.

DR Signal: Amidation; Glycoprotein; Calcium-binding; Phosphorylation; KX Polymorphism; 3D-structure; Antibiotic; Fungicide.

FT SIGNAL 1 18

FT CHAIN 1 449 CHROMOGRANIN A.

FT PEPTIDE 19 94 VASOSTATIN-1.

FT PEPTIDE 142 161 CHROMOSTATIN.

FT PEPTIDE 191 212 CHROMACIN.

FT PEPTIDE 266 312 PANCREASTATIN.

FT PEPTIDE 334 347 WE-14.

FT PEPTIDE 362 382 CATESTATIN.

FT MOD_RES 99 99 PHOSPHORYLATION (PARTIAL).

FT MOD_RES 142 142 PHOSPHORYLATION (PARTIAL).

FT MOD_RES 191 191 PHOSPHORYLATION (PARTIAL).

FT MOD_RES 315 315 PHOSPHORYLATION.

FT MOD_RES 390 390

Query Match 9.8%; Score 88.5; DB 1; Length 449;

Best Local Similarity 24.4%; Pred. No. 6.4;

Matches 39; Conservative 19; Mismatches 57; Indels 45; Gaps 8;

